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OM protein - protein search, using sw model

Run on: June 24, 2004, 15:54:37; Search time 63.95 Seconds

(without alignments)

4069.212 Million cell updates/sec

Title: US-10-054-680-2

Perfect score: 4797

Sequence: 1 MAWLRLQPLTSAFLHFGLVT.....LWLLYILFATLEAYCYIKGF 921

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Database :

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		% Query					
No.	Score		Length	DB	ID	Description	
1	4797	100.0	921	5	ABP74104	Abp74104 Human TRI	
2	4797	100.0	921	5	ABB83246	Abb83246 Human tra	
3	4797	100.0	921	5	ABB81913	Abb81913 Human ion	
4	4790	99.9	921	5	ABB81915	Abb81915 Human ion	
5	4786.5	99.8	922	5	ABB81916	Abb81916 Human ion	
6	4784	99.7	927	5	AAM47745	Aam47745 Human nat	
7	4779.5	99.6	922	5	ABB81917	Abb81917 Human ion	
8	4686	97.7	927	5	ABB83247	Abb83247 Human tra	
9	4671	97.4	925	6	ABU12042	Abu12042 Human NOV	

10	4644	96.8	895	6	ABU12043	Abu12043	Human NOV
11	4505.5	93.9	928	6	ABU12041	Abu12041	Human NOV
12	3425.5	71.4	970	5	AAE18291	Aae18291	Bovine NC
13	3373.5	70.3	921	7	AAO27170	Aao27170	Human 465
14	3373.5	70.3	952	3	AAB41497	Aab41497	Human ORF
15	3093	64.5	595	6	ABR40134	Abr40134	Human 690
16	3093	64.5	620	5	ABB81914	Abb81914	Human ion
17	2143.5	44.7	609	4	AAM13701	Aam13701	Peptide #
18	2143.5	44.7	609	4	ABB32633		Peptide #
19	2143.5	44.7	609	4	AAM26102		Peptide #
20	2143.5	44.7	609	4	ABB18131	Abb18131	Protein #
21	2143.5	44.7	609	4	AAM53461	Aam53461	Human bra
22	2143.5	44.7	609	4	ABG47486	Abg47486	Human liv
23	2143.5	44.7	609	5	ABG35474	Abg35474	Human pep
24	2130.5	44.4	950	4	ABB61721	Abb61721	Drosophil
25	1607	33.5	394	4	ABG26781		Novel hum
26	1607	33.5	394	6	ABO00862	Abo00862	Polypepti
27	599	12.5	120	4	AA005893	Aao05893	Human pol
28	579	12.1	539	3	AAY58044	Aay58044	Arabidops
29	424	8.8	91	4	AAM14216	Aam14216	Peptide #
30	424	8.8	91	4	ABB33163	Abb33163	Peptide #
31	424	8.8	91	4	AAM26626	Aam26626	Peptide #
32	424	8.8	91	4	ABB27991	Abb27991	Human pep
33	424	8.8	91	4	ABB18628	Abb18628	Protein #
34	424	8.8	91	4	AAM66347	Aam66347	Human bon
35	424	8.8	91	4	AAM53959	Aam53959	Human bra
36	424	8.8	91	4	ABG48013	Abg48013	Human liv
37	424	8.8	91	4	AAM01948	Aam01948	Peptide #
38	424	8.8	91	5	ABG35995	Abg35995	Human pep
39	349	7.3	123	4	AAM23946	Aam23946	Rat EST e
40	258.5	5.4	644	7	ADE31661	Ade31661	Human 692
41	251.5	5.2	106	6	ABR40136	Abr40136	69039 pro
42	244.5	5.1	630	5	ABP69673	Abp69673	Human pol
43	239.5	5.0	618	4	AAM78712	Aam78712	Human pro
44	239.5	5.0	661	5	ABB84485	Abb84485	Human NCK
45	239.5	5.0	661	6	AA029752	Aao29752	Human 577

ALIGNMENTS

```
RESULT 1
ABP74104
    ABP74104 standard; protein; 921 AA.
ID
XX
AC
    ABP74104;
XX
    30-JAN-2003 (first entry)
DT
XX
DE
    Human TRICH SEQ ID NO 9.
XX
KW
    Human; TRICH; transporter and ion channel; transport disorder;
KW
     cystic fibrosis; diabetes mellitus; Parkinson's disease; cancer;
KW
     neurological disorder; Alzheimer's disease; Huntington's disease;
     immunological disorder; AIDS; asthma; cell proliferative disorder;
KW
KW
     transgenic; gene therapy; neuroprotective; antidiabetic; cytostatic;
KW
     antiparkinsonian; hypotensive; nootropic; antianaemic; anticonvulsant;
```

KW cerebroprotective; cardiant; anti-HIV; human immunodeficiency virus; KW antiasthmatic; antiatherosclerotic; antigout; antiarteriosclerotic; KW hepatotropic; antiinflammatory; virucide; cytostatic. XX os Homo sapiens. XX WO200246415-A2. PN XX PD 13-JUN-2002. XX 05-DEC-2001; 2001WO-US046963. PFXX 08-DEC-2000; 2000US-0254303P. PR PR 15-DEC-2000; 2000US-0256190P. PR 21-DEC-2000; 2000US-0257504P. 12-JAN-2001; 2001US-0261546P. PR 19-JAN-2001; 2001US-0262832P. PR 26-JAN-2001; 2001US-0264377P. PR PR 02-FEB-2001; 2001US-0266019P. XX PA (INCY-) INCYTE GENOMICS INC. XX PΙ Lee EA, Baughn MR, Yue H, Ding L, Raumann BE, Hafalia AJA; Khan FA, Nguyen DB, Elliott VS, Ramkumar J, Walia NK, Ison CH; PΙ PI Lu Y, Gandhi AR, Warren BA, Duggan BM, Tribouley CM, Burford N; Lu DAM, Lal PG, Yao MG, Xu Y, Bruns CM, Thangavelu K, Swarnakar A; PΙ PΙ Tang YT, Azimzai Y, Thornton M, Arvizu C, Policky JL; XX DR WPI; 2002-519667/55. DR N-PSDB; ABZ33735. XX PΤ Novel human transporter and ion channel polypeptide, useful in diagnosis, PTprevention or treatment of transport, neurological, muscle, immunological PTand cell proliferative disorders. XX PS Claim 64; SEQ ID NO 9; 146pp + Sequence Listing; English. XX CC The invention relates to human transporter and ion channel polypeptide CC (TRICH) (I) selected from one of 32 polypeptide sequences (ABP74096-CC ABP74127), a naturally occurring polypeptide comprising a sequence having CC at least sequence 90 % identity to (I) or a biologically active or CC immunogenic fragment of (I). (I) is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound that CC CC specifically binds (I) or modulates the activity of (I) and for preparing CC a polyclonal or monoclonal antibody by hybridoma technology. CC Polynucleotides (II, ABZ33727-ABZ33758) encoding (I) are useful for CC screening a compound altering gene expression. (I) and (II) are useful in CC a diagnostic tests for a condition or a disease associated with the CC expression of TRICH in a biological sample, especially disorders selected CC from a transport disorder such as cystic fibrosis, diabetes mellitus, CC Parkinson's disease, cardiac disorders, neurological disorders such as CC Alzheimer's disease, Huntington's disease, muscle disorders, CC immunological disorder such as AIDS, asthma and atherosclerosis, and cell CC proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis and CC cancer. (II) is useful for creating knock-in humanised animals or CC transgenic animals to model human diseases, in somatic or germline gene CC therapy, to generate a transcript image of a tissue or cell type, for

CC detecting differences in the chromosomal location due to translocation,
CC inversion among normal, carrier or affected individuals and for mapping
CC genomic sequences. Note: The sequence data for this patent is not
CC represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 921 AA;

Query Match 100.0%; Score 4797; DB 5; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qу	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61		120
Qу	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121		180
Qу	181	IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181		240
Qу	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qу	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR	360
Db	3.01	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR	360
Qу	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qу	421	KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF	480
Db	421	KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF	480
Qу	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qу	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV	600
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV	600
Qу	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL	660
Db	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL	660
Qу	661	${\tt EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS}$	720

```
Db
        661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDOFMEAITVSAAGDEDEDESGEERLPS 720
        721 CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780
Qу
            721 CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780
Db
Qy
        781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840
            Db
        781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840
Qу
        841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900
            Db
        841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900
        901 SLWLLYILFATLEAYCYIKGF 921
Qу
            1111111111111111111
Db
        901 SLWLLYILFATLEAYCYIKGF 921
RESULT 2
ABB83246
ID.
    ABB83246 standard; protein; 921 AA.
XX
AC
    ABB83246;
XX
    21-AUG-2002 (first entry)
DT
XX
DE
    Human transporter protein.
XX
KW
    Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
KW
    spleen; testis; leukocyte; foetal brain; chromosome 14.
XX
os
    Homo sapiens.
XX
    WO200233086-A2.
PN
XX
PD
    25-APR-2002.
XX
    17-OCT-2001; 2001WO-US032152.
PF
XX
    17-OCT-2000; 2000US-0240836P.
PR
    13-MAR-2001; 2001US-00804474.
PR
XX
PA
    (PEKE ) PE CORP NY.
XX
    Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;
PΙ
PΙ
    Beasley EM;
XX
DR
    WPI; 2002-479677/51.
DR
    N-PSDB; ABN83428, ABN83429.
XX
PT
    Human transporter peptide related to sodium/calcium exchanger subfamily
PT
    for identifying modulators useful for treating a disease or condition
PT
    mediated by human transporter protein.
XX
PS
    Claim 1; Fig 2; 200pp; English.
```

```
XX
CC
    The present sequence is a human transporter protein, which is related to
CC
    the sodium/calcium exchanger subfamily. Experimental data indicates
    expression of the transporter gene in humans in brain, heart, kidney,
CC
CC
    lung, spleen, testis, leukocyte and foetal brain. The gene of the
CC
    transporter was mapped to chromosome 14 by ePCR
XX
SO
    Sequence 921 AA;
 Query Match
                    100.0%; Score 4797; DB 5;
                                          Length 921;
                    100.0%; Pred. No. 0;
 Best Local Similarity
 Matches 921; Conservative
                         0; Mismatches
                                          Indels
                                                           0;
                                       0;
                                                  0:
                                                    Gaps
         1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGONNESCSGSSDCKEGVIL 60
Qу
          1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGONNESCSGSSDCKEGVIL 60
Db
        61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPNGE 120
Qу
           61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Db
       121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Qy
           121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Db
       181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qy
           181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVOVWEGLLTLFF 240
Db
       241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qy
          Db
       241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
       301 LVPLEGKEVDESRREMIRILKDLKOKHPEKDLDOLVEMANYYALSHOOKSRAFYRIOATR 360
Qy
          Db
       301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
       361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYOCLENCGAVLLTVVR 420
Qу
           361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Db
       421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Qy
          421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Db
       481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qу
          481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Db
       541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Qу
          541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Db
Qу
       601 KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL 660
```

601 KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL 660

Db

```
Qу
        661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720
            Db
        661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720
        721 CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780
Qу
            Db
        721 CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780
        781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840
Qv
            781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840
Db
        841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900
Qy
            Db
        841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900
Qу
        901 SLWLLYILFATLEAYCYIKGF 921
            901 SLWLLYILFATLEAYCYIKGF 921
Db
RESULT 3
ABB81913
    ABB81913 standard; protein; 921 AA.
XX
AC
    ABB81913;
XX
    09-OCT-2002 (first entry)
DT
XX
DE
    Human ion exchanger protein #1.
XX
KW
    Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW
    antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral.
XX
OS
    Homo sapiens.
XX
PN
    WO200259316-A2.
XX
PD
    01-AUG-2002.
XX
PF
    22-JAN-2002; 2002WO-US001817.
XX
PR
    23-JAN-2001; 2001US-0263384P.
XX
PA
    (LEXI-) LEXICON GENETICS INC.
XX
PΙ
    Friddle CJ, Hilbun E;
XX
DR
    WPI; 2002-599791/64.
DR
    N-PSDB; ABO78861.
XX
PT
    Novel polynucleotides encoding human ion exchanger proteins that are
PT
    structurally related to mammalian sodium-calcium exchanger proteins,
PT
    useful for drug screening, diagnosis and in gene therapy of biological
PT
    disorders.
XX
PS
    Claim 2; Page 37-39; 42pp; English.
```

```
XX
CC
    The invention relates to a novel human ion exchanger protein (NHIEP),
CC
    that shares structural similarity with mammalian sodium-calcium exchanger
CC
    proteins, and potassium dependent versions of the same. The NHIEP of the
CC
    invention has nootropic, cytostatic, antiarthritic, and virucide
CC
    activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC
    be targeted by drugs, oligos, antibodies etc., in order to treat disease
    or to therapeutically augment the efficacy of chemotherapeutic agents
CC
    used in the treatment of cancer, arthritis, or as antiviral agents. The
CC
CC
    sequence represents a NHIEP of the invention
XX
SO
    Sequence 921 AA;
 Query Match
                     100.0%;
                            Score 4797; DB 5;
                                             Length 921;
 Best Local Similarity
                     100.0%;
                            Pred. No. 0;
 Matches 921; Conservative
                           0; Mismatches
                                                     0;
                                          0;
                                             Indels
                                                               0;
                                                         Gaps
          1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
Qy
           Db
          1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
         61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Qу
           61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Db
        121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Qу
           121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Db
        181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVOVWEGLLTLFF 240
Qу
           181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Db
Qy
        241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
           241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Db
        301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Qу
           301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Db
Qу
        361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
           361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Db
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421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480

481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600

541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600

Qу

Db

Qу

Db

Qy

Db

```
601 KIVDEEEYEROENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL 660
Qу
            601 KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL 660
Db
        661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDOFMEAITVSAAGDEDEDESGEERLPS 720
Qу
            661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDOFMEAITVSAAGDEDEDESGEERLPS 720
Db
        721 CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780
Qy
            721 CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780
Db
        781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840
Qу
           781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840
Db
        841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900
Qy
           Db
        841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900
Qy
        901 SLWLLYILFATLEAYCYIKGF 921
           Db
        901 SLWLLYILFATLEAYCYIKGF 921
RESULT 4
ABB81915
    ABB81915 standard; protein; 921 AA.
XX
AC
    ABB81915;
XX
DT
    09-OCT-2002 (first entry)
XX
DE
    Human ion exchanger protein #1 Asp/Gly mutant.
XX
KW
    Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW
    antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW
    mutant; mutein.
XX
os
    Homo sapiens.
os
    Synthetic.
XX
FΗ
    Key
                 Location/Qualifiers
FT
    Misc-difference 630
FT
                 /note= "Wild-type Asp substituted by Gly"
XX
PN
    WO200259316-A2.
XX
PD
    01-AUG-2002.
XX
PF
    22-JAN-2002; 2002WO-US001817.
XX
PR
    23-JAN-2001; 2001US-0263384P.
XX
PA
    (LEXI-) LEXICON GENETICS INC.
XX
ΡI
    Friddle CJ, Hilbun E;
```

XX DR WPI; 2002-599791/64. XX PTNovel polynucleotides encoding human ion exchanger proteins that are PTstructurally related to mammalian sodium-calcium exchanger proteins, PTuseful for drug screening, diagnosis and in gene therapy of biological PΤ disorders. XX PS Disclosure; Page; 42pp; English. XX CC The invention relates to a novel human ion exchanger protein (NHIEP), that shares structural similarity with mammalian sodium-calcium exchanger CC proteins, and potassium dependent versions of the same. The NHIEP of the CC CC invention has nootropic, cytostatic, antiarthritic, and virucide activity. The polynucleotide may have a use in gene therapy. NHIEPs can CC CC be targeted by drugs, oligos, antibodies etc., in order to treat disease CC or to therapeutically augment the efficacy of chemotherapeutic agents used in the treatment of cancer, arthritis, or as antiviral agents. The CC sequence represents a mutant form of a NHIEP of the invention. Note: The CC present sequence is not shown in the specification but is derived from CC CC the human NHIEP sequence shown as SEQ ID 2 (ABB81913) XX SO Sequence 921 AA; Query Match 99.98; Score 4790; DB 5; Length 921; Best Local Similarity 99.9%; Pred. No. 0: Matches 920; Conservative 0; Mismatches 1; Indels Gaps 0; Qy 1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGONNESCSGSSDCKEGVIL 60 Db 1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60 61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120 Qy 61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPNGE 120 Db 121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180 Qy 121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180 Db 181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240 Qy Db 181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240 241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300 Qy 241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300 Db 301 LVPLEGKEVDESRREMIRILKDLKOKHPEKDLDOLVEMANYYALSHOOKSRAFYRIOATR 360 Qу 301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360 Db Qу 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYOCLENCGAVLLTVVR 420 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420 Db

421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480

Qy

```
421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETOKEFSVGIIDDDIFEEDEHF 480
Db
        481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qy
           481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Db
        541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Qу
           541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Db
       601 KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL 660
Qу
           Db
       601 KIVDEEEYERQENFFIALGEPKWMERGISGVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL 660
       661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720
Qу
           Db
       661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDOFMEAITVSAAGDEDEDESGEERLPS 720
       721 CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780
Qу
           721 CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780
Db
Qу
       781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840
           781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840
Db
       841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900
Qу
           841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900
Db
       901 SLWLLYILFATLEAYCYIKGF 921
Qу
           Db
       901 SLWLLYILFATLEAYCYIKGF 921
RESULT 5
ABB81916
   ABB81916 standard; protein; 922 AA.
XX
AC
   ABB81916;
XX
   09-OCT-2002 (first entry)
DT
XX
DE
   Human ion exchanger protein #1 Ala mutant.
XX
KW
   Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW
    antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW
   mutant; mutein.
XX
OS
   Homo sapiens.
OS
   Synthetic.
XX
FH
   Key
                Location/Qualifiers
FT
   Misc-difference 704. .705
FT
                /note= "Wild-type Ala Ala substituted by Ala Ala Ala"
XX
```

```
PN
    WO200259316-A2.
XX
PD
    01-AUG-2002.
XX
PF
    22-JAN-2002; 2002WO-US001817.
XX
PR
    23-JAN-2001; 2001US-0263384P.
XX
PA
    (LEXI-) LEXICON GENETICS INC.
XX
    Friddle CJ, Hilbun E;
PΙ
XX
DR
    WPI; 2002-599791/64.
XX
PΤ
    Novel polynucleotides encoding human ion exchanger proteins that are
PT
    structurally related to mammalian sodium-calcium exchanger proteins,
PT
    useful for drug screening, diagnosis and in gene therapy of biological
PΤ
    disorders.
XX
PS
    Disclosure; Page; 42pp; English.
XX
CC
    The invention relates to a novel human ion exchanger protein (NHIEP),
CC
    that shares structural similarity with mammalian sodium-calcium exchanger
CC
    proteins, and potassium dependent versions of the same. The NHIEP of the
CC
    invention has nootropic, cytostatic, antiarthritic, and virucide
CC
    activity. The polynucleotide may have a use in gene therapy. NHIEPs can
    be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC
CC
    or to therapeutically augment the efficacy of chemotherapeutic agents
CC
    used in the treatment of cancer, arthritis, or as antiviral agents. The
CC
    sequence represents a mutant form of a NHIEP of the invention. Note: The
CC
    present sequence is not shown in the specification but is derived from
CC
    the human NHIEP sequence shown as SEQ ID 2 (ABB81913)
XX
SQ
    Sequence 922 AA;
 Query Match
                       99.8%;
                             Score 4786.5; DB 5;
                                                 Length 922;
 Best Local Similarity
                      99.9%; Pred. No. 0;
 Matches 921; Conservative
                           0; Mismatches
                                             0; Indels
                                                         1;
                                                            Gaps
                                                                   1;
Qу
          1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
            Db
          1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
Qу
         61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPNGE 120
            61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Db
Qy
        121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
            121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Db
Qy
        181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVOVWEGLLTLFF 240
            Db
        181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qу
        241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
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Db
       241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
       301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Qу
          301 LVPLEGKEVDESRREMIRILKDLKOKHPEKDLDQLVEMANYYALSHOOKSRAFYRIQATR 360
Db
       361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYOCLENCGAVLLTVVR 420
Qу
          361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Db
       421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Qу
          421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETOKEFSVGIIDDDIFEEDEHF 480
Db
       481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qу
          481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Db
       541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Qу
          Db
       541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
       601 KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL 660
Qу
          Db
       601 KIVDEEEYEROENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL 660
Qу
       661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVS-AAGDEDEDESGEERLP 719
          Db
       661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAAGDEDEDESGEERLP 720
       720 SCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGL 779
Qу
          721 SCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGL 780
Db
Qу
       780 KDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAI 839
          781 KDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAI 840
Db
Qу
       840 YWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLF 899
          841 YWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLF 900
Db
       900 VSLWLLYILFATLEAYCYIKGF 921
Qу
          901 VSLWLLYILFATLEAYCYIKGF 922
Db
RESULT 6
AAM47745
   AAM47745 standard; protein; 927 AA.
XX
AC
   AAM47745;
XX
DT
   25-FEB-2002 (first entry)
XX
DE
   Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3.
```

XX

```
KW
    Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;
    cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;
KW
    myocarditis; pulmonary hypertension; cardiotoxicity; cardiant; Vaccine;
KW
    coronary heart disease; renal failure; ischaemic disorder;
KW
    Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder.
KW
XX
os
    Homo sapiens.
XX
PN
    WO200183744-A2.
XX
PD
    08-NOV-2001.
XX
PF
    30-APR-2001; 2001WO-EP004886.
XX
    02-MAY-2000; 2000EP-00109080.
PR
XX
PA
    (MERE ) MERCK PATENT GMBH.
XX
PΙ
    Wilm C;
XX
DR
    WPI; 2002-041493/05.
DR
    N-PSDB; ABA04756.
XX
PT
    New polypeptide, useful as vaccines for inducing immune response against
PT
    diseases such as myocardial infarction, arrhythmia, ischemic disorders,
PT
    renal disorders in mammal.
XX
PS
    Claim 1; Page 38-41; 41pp; English.
XX
CC
    The present sequence is the protein sequence for human Natrium(+)-Calcium
CC
    (2+) exchanger form 3 (HNCX3). The HNCX3 gene maps to human chromosome
CC
    14. HNCX3 and its coding sequence are useful for treating acute and
CC
    chronic cardiac failure of different aetiologies, myocardial infarction,
CC
    cardiac hypertrophy, arrhythmia, myocarditis, pulmonary hypertension,
    cardiotoxicity (e.g. induced by chemotherapy), coronary heart disease,
CC
CC
    acute and chronic renal failure, ischaemic disorders of skeletal muscle
CC
    and ischaemic brain disorders of different aetiologies
XX
SO
    Sequence 927 AA;
 Query Match
                        99.7%;
                               Score 4784; DB 5; Length 927;
 Best Local Similarity
                        99.4%; Pred. No. 0;
 Matches 921; Conservative
                              0; Mismatches
                                               0; Indels
                                                            6;
                                                                Gaps
                                                                       1;
           1 MAWLRLOPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGONNESCSGSSDCKEGVIL 60
Qу
             1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
Db
Qу
          61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
             Db
          61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPNGE 120
Qу
         121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
             Db
         121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
         181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qу
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Db	181	IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qу	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Db	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qу	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Db	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Db	361	
Qу	421	KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Db	421	
Qу	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Db	481	
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Db	541	
Qy	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVL 654
Db	601	
Qy	655	GEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 714
Db	661	
Qy	715	EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFG 774
Db	721	
Qу	775	CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 834
Db	781	
Qу	835	SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLA 894
Db	841	
Qу	895	TTWLFVSLWLLYILFATLEAYCYIKGF 921
Db	901	

RESULT 7 ABB81917

ID ABB81917 standard; protein; 922 AA.

XX

AC ABB81917;

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XX
DT
     09-OCT-2002 (first entry)
XX
DE
     Human ion exchanger protein #1 Asp/Gly+Ala mutant.
XX
KW
     Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW
     antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW
    mutant; mutein.
XX
os
     Homo sapiens.
OS
     Synthetic.
XX
FH
                     Location/Qualifiers
     Key
FT
    Misc-difference 630
FΤ
                     /note= "Wild-type Asp substituted by Gly"
FT
    Misc-difference 704. .705
FT
                     /note= "Wild-type Ala Ala substituted by Ala Ala Ala"
XX
PN
    WO200259316-A2.
XX
PD
     01-AUG-2002.
XX
PF
     22-JAN-2002; 2002WO-US001817.
XX
PR
     23-JAN-2001; 2001US-0263384P.
XX
PA
     (LEXI-) LEXICON GENETICS INC.
XX
PΙ
    Friddle CJ, Hilbun E;
XX
    WPI; 2002-599791/64.
DR
XX
PT
    Novel polynucleotides encoding human ion exchanger proteins that are
PΤ
     structurally related to mammalian sodium-calcium exchanger proteins,
PT
     useful for drug screening, diagnosis and in gene therapy of biological
PT
     disorders.
XX
PS
     Disclosure; Page; 42pp; English.
XX
    The invention relates to a novel human ion exchanger protein (NHIEP),
CC
CC
     that shares structural similarity with mammalian sodium-calcium exchanger
CC
    proteins, and potassium dependent versions of the same. The NHIEP of the
CC
     invention has nootropic, cytostatic, antiarthritic, and virucide
CC
    activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC
    be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC
    or to therapeutically augment the efficacy of chemotherapeutic agents
CC
     used in the treatment of cancer, arthritis, or as antiviral agents. The
CC
     sequence represents a mutant form of a NHIEP of the invention. Note: The
CC
    present sequence is not shown in the specification but is derived from
CC
     the human NHIEP sequence shown as SEQ ID 2 (ABB81913)
XX
SO
     Sequence 922 AA;
  Query Match
                          99.6%; Score 4779.5; DB 5; Length 922;
  Best Local Similarity
                          99.8%; Pred. No. 0;
 Matches 920; Conservative
                                 0; Mismatches
                                                   1; Indels
                                                                 1; Gaps
                                                                              1;
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Qy ·		MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	
Db	1	${\tt MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL}$	60
Qу	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qу	181	IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qу	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241		300
Qy	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361		420
Qу	421	~ · · · · · · · · · · · · · · · · · · ·	480
Db	421		480
Qу	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481		540
Qу	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV	600
Db	541		600
QУ	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL	660
Db	601		660
Qу	661	EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVS-AAGDEDEDESGEERLP	719
Db	661		720
Qу	720	SCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGL	779
Db	721		780
Qу	780	KDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAI	839
Db	781		840
Qу	840	YWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLF	899

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Db
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         900 VSLWLLYILFATLEAYCYIKGF 921
Qу
             11111111111111111111111
Db
         901 VSLWLLYILFATLEAYCYIKGF 922
RESULT 8
ABB83247
    ABB83247 standard; protein; 927 AA.
XX
AC
    ABB83247;
XX
DT
    21-AUG-2002 (first entry)
XX
DE
    Human transporter protein-related protein, used in a homology alignment.
XX
KW
    Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
KW
    spleen; testis; leukocyte; foetal brain; chromosome 14.
XX
OS
    Unidentified.
XX
PN
    W0200233086-A2.
XX
PD
    25-APR-2002.
XX
PF
    17-OCT-2001; 2001WO-US032152.
XX
    17-OCT-2000; 2000US-0240836P.
PR
    13-MAR-2001; 2001US-00804474.
PR
XX
PA
    (PEKE ) PE CORP NY.
XX
ΡI
    Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;
PΙ
    Beasley EM;
XX
DR
    WPI; 2002-479677/51.
XX
PT
    Human transporter peptide related to sodium/calcium exchanger subfamily
PT
     for identifying modulators useful for treating a disease or condition
PT
    mediated by human transporter protein.
XX
PS
    Disclosure; Fig 2; 200pp; English.
XX
CC
    The present invention relates to a human transporter protein, which is
CC
    related to the sodium/calcium exchanger subfamily (ABB83246).
    Experimental data indicates expression of the transporter gene in humans
CC
    in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal
CC
CC
    brain. The gene of the transporter was mapped to chromosome 14 by ePCR.
    The present protein was used in a sequence alignment with the transporter
CC
CC
    protein to illustrate the invention
XX
SQ
    Sequence 927 AA;
  Query Match
                         97.7%; Score 4686; DB 5; Length 927;
```

Best Local Similarity 96.8%; Pred. No. 0;

	Matches 89	7; Conservative	e 14;	Mismatches	10;	Indels	6;	Gaps	1;
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Dł) 1	MAWLRLQPLTSAFL							60
Q	y 61	PIWYPENPSLGDKI							120
Dh	61	PIWYPENPSLGDKIA							120
Q	, 121	TSTTTIRVWNETVS							180
Dk	121	TSTTTIRVWNETVS							180
Q	7 181	IIGICVYVIPDGETI				-			240
Dk	181	IIGICVYVIPDGETI							240
Q	7 241	FPVCVLLAWVADKRI							300
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Q	301	LVPLEGKEVDESRR							360
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Q	361	MMTGAGNILKKHAAI							420
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Q	421	KGGDMSKTMYVDYKT							480
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Q	481	FVRLSNVRIEEEQPE							540
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Q	541	VSESIGVMEVKVLR							600
Db	541	VSESIGVMEVKVLR							600
Q	601	KIVDEEEYERQENFI							654
Dk	601	KIVDEEEYERQENF							660
Q	7 655	GEHPKLEVIIEESYE							714
Dh	661	GEHPKLEVIIEESY							720
Q	715	EERLPSCFDYVMHFI							774
Dk	721	EERLPSCFDYVMHFI							780
Q	775	CTIGLKDSVTAVVFV							834
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              Db
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DT
     19-FEB-2003 (first entry)
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     NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
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     metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW
     antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
     cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW
KW
     anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
KW
     Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW
     metabolic syndrome X; wasting disease.
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OS
     Homo sapiens.
XX
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     W0200281625-A2.
XX
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     17-OCT-2002.
XX
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     03-APR-2002; 2002WO-US010366.
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     03-APR-2001; 2001US-0281086P.
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     25-APR-2001; 2001US-0286292P.
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     07-JUN-2001; 2001US-0296692P.
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     26-JUN-2001; 2001US-0300883P.
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     08-AUG-2001; 2001US-0311003P.
     13-AUG-2001; 2001US-0311973P.
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     16-AUG-2001; 2001US-0312901P.
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     14-SEP-2001; 2001US-0322283P.
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     05-OCT-2001; 2001US-0327448P.
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    04-FEB-2002; 2002US-0354391P.
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    02-APR-2002; 2002US-00114153.
PR
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     (CURA-) CURAGEN CORP.
XX
                 Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
PΙ
    Padigaru M,
    Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
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    Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
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    Peyman JA, Catterton E, Macdougall JR,
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ΡI
    Mazur A;
XX
    WPI: 2003-046862/04.
DR
    N-PSDB; ABX56262.
DR
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PT
    New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT
    atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT
    disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT
XX
PS
    Claim 1; Page 85; 425pp; English.
XX
    This invention describes novel polypeptides, termed NOVX which have
CC
    antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC
CC
    neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC
    cardiant and immunomodulatory activity. The polypeptide and any
CC
    antibodies generated from it are useful in the manufacture of a
    medicament for treating a syndrome associated with a human disease
CC
CC
    selected from a pathology associated with the NOVX polypeptide. Fragments
CC
    and portions of the polynucleotides encoding NOVX polypeptides are useful
CC
    to map the location of NOVX genes on a chromosome, to identify
CC
    individuals from minute biological samples, as DNA markers for
CC
    restriction fragment length polymorphism (RFLP), and are useful to
CC
    prepare polymerase chain reaction primers. The products of the invention
CC
    can be used in gene therapy and for treating cardiomyopathy, metabolic
CC
    disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC
    anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC
    disease, immune disorders, haematopoietic disorders, and various
CC
    dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC
    syndrome X and wasting disorders associated with chronic diseases and
CC
    various cancers. ABU12041-ABU12086 represent the polypeptide fragments
    encoded by the NOVX polynucleotides represented in ABX56261-ABX56306
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             1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
Db
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Qу
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Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR	360
Qу	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qу	421	KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF	480
Db	421	KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
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Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIHI	600
Qу	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGE	656
Db	601	KVIDDEAYEKNKNYFIEMMGPRMVDMSFQKALLLSPDRKLTMEEEEAKRIAEMGKPVLGE	660
QУ	657	HPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEE	716
Db	661	HPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEE	720
Qу	717	RLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCT	776
Db	721	RLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCT	780
Qу	777	IGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSV	836
Db	781	IGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSV	840
Qу	837	AAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATT	896
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ДÄ	897	WLFVSLWLLYILFATLEAYCYIKGF 921	
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XX
AC
     ABU12043;
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DT
     19-FEB-2003
                 (first entry)
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     NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
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     metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW
     antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW
     cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
     anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
KW
KW
     Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW
     metabolic syndrome X; wasting disease.
XX
os
     Homo sapiens.
XX
PN
     WO200281625-A2.
XX
PD
     17-OCT-2002.
XX
PF
     03-APR-2002; 2002WO-US010366.
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     03-APR-2001; 2001US-0281086P.
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     06-APR-2001; 2001US-0282020P.
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PA
     (CURA-) CURAGEN CORP.
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     Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
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Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
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    Peyman JA, Catterton E, Macdougall JR, Edinger SR,
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                                                        Stone DJ;
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    Mazur A;
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DR
    WPI; 2003-046862/04.
DR
    N-PSDB; ABX56263.
XX
    New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT
PT
    atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT
    disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT
    cancer.
XX
PS
    Claim 1; Page 86; 425pp; English.
XX
CC
    This invention describes novel polypeptides, termed NOVX which have
CC
    antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC
    neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC
    cardiant and immunomodulatory activity. The polypeptide and any
CC
    antibodies generated from it are useful in the manufacture of a
CC
    medicament for treating a syndrome associated with a human disease
CC
    selected from a pathology associated with the NOVX polypeptide. Fragments
CC
    and portions of the polynucleotides encoding NOVX polypeptides are useful
    to map the location of NOVX genes on a chromosome, to identify
CC
CC
    individuals from minute biological samples, as DNA markers for
CC
    restriction fragment length polymorphism (RFLP), and are useful to
CC
    prepare polymerase chain reaction primers. The products of the invention
CC
    can be used in gene therapy and for treating cardiomyopathy, metabolic
CC
    disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC
    anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC
    disease, immune disorders, haematopoietic disorders, and various
CC
    dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC
    syndrome X and wasting disorders associated with chronic diseases and
CC
    various cancers. ABU12041-ABU12086 represent the polypeptide fragments
    encoded by the NOVX polynucleotides represented in ABX56261-ABX56306
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             122 LSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFITAAW 181
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         210 SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDK 269
Qу
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182 SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDK 241
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       390 EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFT 449
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          362 EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFT 421
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          602 DVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGT 661
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       690 HSWRDOFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGW 749
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          662 HSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGW 721
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          782 YADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVC 841
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       870 ISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
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DT
   19-FEB-2003
             (first entry)
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DE
   Human NOV1a CG56258-01 protein SEQ ID 2.
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     metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
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     antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
     cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW
KW
     anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
KW
     Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW
     metabolic syndrome X; wasting disease.
XX
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     Homo sapiens.
XX
PN
    WO200281625-A2.
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     17-OCT-2002.
XX
     03-APR-2002; 2002WO-US010366.
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    WPI; 2003-046862/04.
DR
    N-PSDB; ABX56261.
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PT
    New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT
     atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT
     disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
```

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РΤ
    cancer.
XX
PS
    Claim 1; Page 84; 425pp; English.
XX
CC
    This invention describes novel polypeptides, termed NOVX which have
CC
    antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC
    neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC
    cardiant and immunomodulatory activity. The polypeptide and any
CC
    antibodies generated from it are useful in the manufacture of a
CC
    medicament for treating a syndrome associated with a human disease
CC
    selected from a pathology associated with the NOVX polypeptide. Fragments
    and portions of the polynucleotides encoding NOVX polypeptides are useful
CC
    to map the location of NOVX genes on a chromosome, to identify
CC
CC.
    individuals from minute biological samples, as DNA markers for
CC
    restriction fragment length polymorphism (RFLP), and are useful to
CC
    prepare polymerase chain reaction primers. The products of the invention
CC
    can be used in gene therapy and for treating cardiomyopathy, metabolic
CC
    disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC
    anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC
    disease, immune disorders, haematopoietic disorders, and various
CC
    dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC
    syndrome X and wasting disorders associated with chronic diseases and
CC
    various cancers. ABU12041-ABU12086 represent the polypeptide fragments
CC
    encoded by the NOVX polynucleotides represented in ABX56261-ABX56306
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SQ
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 Query Match
                      93.9%; Score 4505.5; DB 6;
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 Best Local Similarity
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                            37; Mismatches
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                                                                    3;
                                                         9;
                                                             Gaps
Qу
          1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGONNESCSGSSDCKEGVIL 60
            1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGONNESCSGSSDCKEGVIL 60
Db
Qу
         61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPNGE 120
            61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Db
Qу
        121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
            121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Db
        181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qу
            Db
        181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
        241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qy
            241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Db
        301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Qу
            Db
        301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
```

361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qу

```
Db
        361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
        421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Qу
           421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Db
        481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qy
           481 FVRLSNVRIEEEOPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Db
Qу
        541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
           541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTLQV 600
Db
        601 KIVDEEEYERQENFFIALGEPKWMERGISDVT-----DRKLTMEEEEAKRIAEMGKPVL 654
Qу
           11111 11111:111111111
        601 KIVDDEEYEKKDNFFIELGQPQWLKRGISALLLNQGDGDRKLTAEEEEARRIAEMGKPVL 660
Db
        655 GEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 714
Qу
           661 GENCRLEVIIEESYDFKNTVDKLIKKTNLALVIGTHSWREOFLEAITVS-AGDEEEEEDG 719
Db
        715 --EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASH 772
Qу
             Db
        720 SREERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFGVSILVIGLLTALIGDLASH 779
        773 FGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALODVYADASIGNVTGSNAVNVFLGIGL 832
Qу
           Db
        780 FGCTVGLKDSVNAVVFVALGTSIPDTFASKVAALODOCADASIGNVTGSNAVNVFLGLGV 839
        833 AWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCK 892
Qу
           840 AWSVAAVYWAVQGRPFEVRTGTLAFSVTLFTVFAFVGIAVLLYRRRPHIGGELGGPRGPK 899
Db
        893 LATTWLFVSLWLLYILFATLEAYCYIKGF 921
Qу
           1111 11: 11111111:1111:1:11
Db
        900 LATTALFLGLWLLYILFASLEAYCHIRGF 928
RESULT 12
AAE18291
ID
   AAE18291 standard; protein; 970 AA.
XX
AC
   AAE18291;
XX
    07-MAY-2002 (first entry)
DT
XX
DE
    Bovine NCX-1 protein.
XX
KW
    Bovine; recombinant protein; larvae expression system; membrane protein;
KW
    transport protein; cardiac sodium-calcium exchange protein; Na-K ATPase;
KW
    NCX1; cystic fibrosis transmembrane conductance regulator; CFTR; vaccine;
KW
    channel forming protein; junctional protein; conexin 32.
XX
OS
    Bos taurus.
XX
```

PN

W0200206464-A2.

```
XX
         24-JAN-2002.
PD
XX
PF
         09-JUL-2001; 2001WO-US021606.
XX
PR
         13-JUL-2000; 2000US-0218125P.
XX
PA
         (UMOR ) UNIV MISSOURI.
XX
PΙ
        Hale CC, Price EM;
XX
DR
        WPI; 2002-171806/22.
DR
        N-PSDB; AAD24450.
XX .
PT
         Producing recombinant proteins e.g. membrane, transport and channel
PT
         forming proteins in larvae expression system, by infecting larvae with
PT
         vector having a sequence encoding recombinant fusion protein with
PT
         affinity tag.
XX
PS
         Example 1; Page 37-40; 40pp; English.
XX
CC
         The patent discloses methods of producing recombinant proteins in larvae
CC
         expression system, by infecting the larvae with vector having a sequence
CC
         encoding recombinant fusion protein with affinity tag. The methods are
CC
         useful for producing recombinant protein, preferably membrane proteins,
CC
         transport proteins such as NCX1 (cardiac sodium-calcium exchange protein)
CC
         or Na-K ATPase, channel forming proteins such as cystic fibrosis trans-
CC
        membrane conductance regulator (CFTR), junctional protein (conexin 32),
CC
         receptor, cytoskeletal and other membrane associated proteins. They are
CC
         also useful for producing prostate specific membrane antigens and sodium
CC
        phosphate co-transporters from kidney. The methods are also useful for
CC
         producing recombinant fusion proteins in large quantities that are both
CC
         highly homogenous and biologically active. The recombinant proteins
CC
         produced by the methods of the invention can be included as part of a
        pharmaceutical, nutritional, drug or vaccine composition. The present
CC
CC
         sequence is bovine NCX-1 protein
XX
SO
         Sequence 970 AA;
   Query Match
                                              71.4%; Score 3425.5; DB 5; Length 970;
   Best Local Similarity
                                              68.7%; Pred. No. 0;
   Matches 672; Conservative 110; Mismatches 131; Indels
                                                                                                                  65; Gaps
                                                                                                                                       10;
Qv
                     1 MAWLRLOPLTSAFLHFGLVTFVLF--LNGLRAEAGGSGDVPSTGONNESCSGSSDCKEGV 58
                                                : :|| :: : ||
                                                                                          |:
                                                                                                 ||:
                                                                                                                1:11
Db
                     1 MLQFSLSPTLSMGFHVIAMVALLFSHVDHISAETEMEGEGNETGE----CTGSYYCKKGV 56
Qу
                    59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPN 118
                         57 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN 116
Db
Qу
                  119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM 178
                         117 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 176
Db
                  179 FIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL 238
Qу
                         1111 : [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [11]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [11]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [111]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [11]: [
```

Db	177	FIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTF	236
Qу	239	FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSH	295
Db	237	: : :	296
QУ	296	FLDGNLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ	348
Db	297		355
QУ	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC	407
Db	356	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTYQC	415
QУ	408	LENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
Db	416	LENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG	475
QУ	468	IIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD	527
Db	476	IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVSTLACLGSPSTATVTIFDDD	532
ΟУ	528	HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL	587
Db	533	HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL	592
Qу	588	EFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG	627
Db	593	EFQNDEIVKTISVKVIDDEEYEKNKTFFLEIGEPRLVEMSEKKALLLNELGGFTITGKYL	652
Qу	628	ISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVI	663
Db	653	YGQPVFRKVHAREHPLPSTIITIADEYDDKQPLTSKEEEERRIAEMGRPILGEHTRLEVI	712
Qу	664	IEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFD	723
Db	713	IEESYEFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKLPSCFD	772
QУ	724	YVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSV	783
Db	773	YVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFACTIALKDSV	832
Qу	784	TAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWAL	843
Db	833	TAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAA	892
Qу	844	QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLW ::	903
Db	893	NGEQFKVSPGTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSCLFVLLW	952
Qу	904	LLYILFATLEAYCYIKGF 921	
Db	953	LLYIFFSSLEAYCHIKGF 970	

```
ID
     AAO27170 standard; protein; 921 AA.
XX
AC
     AAO27170;
XX
DT
     02-SEP-2003
                 (first entry)
XX
DΕ
     Human 46566 protein (Na-Ca exchanger SLC8).
XX
KW
     Na-Ca exchanger SLC8; 46566; hyperalgesia; allodynia; nociceptive;
     analgesic; neuropathic; fibromyalgia; migraine; arthritis; causalqia;
KW
KW
     chronic fatigue syndrome; neurodystrophy; plantar fasciitis; pain; human.
XX
os
     Homo sapiens.
XX
     WO2003037254-A2.
PN
XX
     08-MAY-2003.
PD
XX
     28-OCT-2002; 2002WO-US034567.
PF
XX
PR
     31-OCT-2001; 2001US-0335078P.
XX
PΑ
     (MILL-) MILLENNIUM PHARM INC.
XX
PΙ
     Silos-Santiago I;
XX
DR
    WPI; 2003-457344/43.
     N-PSDB; AAL55587.
DR
XX
PT
     Identifying compounds that modulate 46566 (Na-Ca exchanger SLC8) nucleic
PT
     acid expression or polypeptide activity, useful for preventing and
PT
     treating pain disorders e.g. inflammatory, chronic, neuropathic and
PT
     cancer pain.
XX
PS
     Disclosure; Fig 1b; 74pp; English.
XX
CC
     This invention relates to novel methods and compositions for the
CC
     diagnosis and treatment of pain disorders. The Na-Ca exchanger SLC8
CC
     referred to herein as 46566, is predominantly expressed in the nervous
CC
     tissues (brain, spinal chord and dorsal root ganglia). Furthermore, it is
CC
     down-regulated in animal models of pain such that there is an altered
CC
     pain response, which manifests as a reduced threshold to noxious stimuli
CC
     (hyperalgesia) and lowered thresholds to innocuous stimuli (allodynia).
CC
     Therefore the 46566 molecule is believed to be involved in nociceptive
CC
    pathways by participating in pain signalling mechanisms and modulating
CC
    pain elicitation, hence it provides a target by which to control pain and
     treat disorders. This invention provides methods to identify analgesic
CC
CC
     compounds that modulate 46566 expression or 46566 activity and
CC
     consequently are capable of treating inflammatory, chronic and/ or
     neuropathic pain. It further provides diagnostic assays, as well as
CC
CC
     prophylatic and therapeutic methods for treating subjects with, for
CC
     example, fibromyalgia, cancer pain, chronic fatigue syndrome, migraine
CC
     pain, arthritis, causalgia, neurodystrophy or plantar fasciitis. This
CC
     polypeptide sequence is the human 46566 protein sequence (Na-Ca exchanger
CC
     SLC8) of the invention
XX
```

SQ

Sequence 921 AA;

Best	Match 70.3%; Score 3373.5; DB 7; Length 921; Local Similarity 71.0%; Pred. No. 0; es 638; Conservative 124; Mismatches 104; Indels 33; Gaps 9,
Qу	40 STGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFM 99
Db	
Qу	100 ASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHG 159
Db	: : : : :
Qу	160 FIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYM 219
Db	: :: : : : : :
Qу	220 ILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEG 279
Db	
Qу	280 DHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQ 334
Db	: :: : :
Qу	335 LVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDF 394
Db	:
Qу	395 ISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVV 454 :: :
Db	393 ASRIFFEPSLYHCLENCGSVLLSVTCQGGEGNSTFYVDYRTEDGSAKAGSDYEYSEGTLV 452
Qу	455 LKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR 510
Db	:
Qy	511 AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVE 570
Db	: : : : : : :: : :
Qу	571 GTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERGISD 630
Db	564 GTARGGGVHYEDACGELEFGDDETMKTLQVKIVDDEEYEKKDNFFIELGQPQWLKRGISA 623
Qу	631 VTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLA 684 :
Db	624 LLLNQGDGDRKLTAEEEEARRIAEMGKPVLGENCRLEVIIEESYDFKNTVDKLIKKTNLA 683
Qу	685 LVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPP 742
Db	684 LVIGTHSWREQFLEAITVS-AGDEEEEEDGSREERLPSCFDYVMHFLTVFWKVLFACVPP 742
Qу	743 TEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASK 802
Db	

```
803 AAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLF 862
Qу
              803 VAALQDQCADASIGNVTGSNAVNVFLGLGVAWSVAAVYWAVQGRPFEVRTGTLAFSVTLF 862
Db
         863 TIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
Qу
             Db
         863 TVFAFVGIAVLLYRRRPHIGGELGGPRGPKLATTALFLGLWLLYILFASLEAYCHIRGF 921
RESULT 14
AAB41497
ID
    AAB41497 standard; protein; 952 AA.
XX
AC
    AAB41497;
XX
DT
    08-FEB-2001 (first entry)
XX
DE
    Human ORFX ORF1261 polypeptide sequence SEQ ID NO:2522.
XX
KW
    Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW
    vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW
    anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW
    immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic;
KW
    hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW
    antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW
    antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW
    neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW
    cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW
    cholesterol ester storage; systemic lupus erythematosus; infection;
KW
    severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW
    allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW
    bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW
    thrombosis; contraceptive.
XX
os
    Homo sapiens.
XX
PN
    WO200058473-A2.
XX
PD
    05-OCT-2000.
XX
PF
    31-MAR-2000; 2000WO-US008621.
XX
PR
    31-MAR-1999;
                   99US-0127607P.
PR
    02-APR-1999;
                   99US-0127636P.
PR
    05-APR-1999;
                  99US-0127728P.
    30-MAR-2000; 2000US-00540763.
PR
XX
PA
    (CURA-) CURAGEN CORP.
XX
PΙ
    Shimkets RA, Leach M;
XX
DR
    WPI; 2000-602362/57.
DR
    N-PSDB; AAC75706.
XX
PT
    Novel nucleic acids and peptides derived from open reading frame X,
PT
    useful for treating e.g. cancers, proliferative disorders,
PT
    neurodegenerative disorders and cardiovascular disease.
```

Claim 11; Page 1809-1812; 5507pp; English.

XX CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, CC which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; CC CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; CC dermatological; immunosuppressive; antiinflammatory; antibacterial; CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The

CC sequences can be used for determining the presence of or predisposition CC to, or preventing or treating pathological conditions associated with an CC ORFX-associated disorder. The nucleic acids can be used to express ORFX

CC proteins in gene therapy vectors. The proteins and nucleic acids may be CC used to treat cancers, proliferative disorders, neurodegenerative

CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,

CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester CC storage, systemic lupus erythematosus, severe combined immunodeficiency CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune

disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to

CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive

SQ Sequence 952 AA;

XX PS

CC

XX

Query Match 70.3%; Score 3373.5; DB 3; Length 952; Best Local Similarity 71.0%; Pred. No. 0; Matches 638; Conservative 124; Mismatches 104; Indels 33; Gaps 9;

Qy 40 STGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFM 99

Db 70 STG----GCQGSYRCQPGVLLPVWEPDDPSLGDKAARAVVYFVAMVYMFLGVSIIADRFM 125

Db 126 AAIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHN 185

Qy 160 FIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYM 219

Qy 220 ILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEG 279

Qy 280 DHPKGIEMDGKMMNSHFLDGNL-----VPLEGKEVDESRREMIRILKDLKQKHPEKDLDQ 334

Db 365 LVGIANYYALLHQQKSRAFYRIQATRLMTGAGNVLRRHAADASRRAAPAEGAGEDE-DDG 423

Db 424 ASRIFFEPSLYHCLENCGSVLLSVTCQGGEGNSTFYVDYRTEDGSAKAGSDYEYSEGTLV 483

```
455 LKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEQ----PEEGMPPAIFNSLPLPR 510
.Qy
            1: 1
        484 FKPGETOKELRIGIIDDDIFEEDEHFFVRLLNLRVGDAOGMFEPDGG-----GRPK 534
Db
Qy
        511 AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVE 570
             1:1:1111111111111:1:
                                  535 GRLVAPLLATVTILDDDHAGIFSFQDRLLHVSECMGTVDVRVVRSSGARGTVRLPYRTVD 594
Db
Qу
        571 GTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERGISD 630
           Db
        595 GTARGGGVHYEDACGELEFGDDETMKTLQVKIVDDEEYEKKDNFFIELGQPQWLKRGISA 654
Qу
        631 VT-----DRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLA 684
                  Db
        655 LLLNQGDGDRKLTAEEEEARRIAEMGKPVLGENCRLEVIIEESYDFKNTVDKLIKKTNLA 714
        685 LVVGTHSWRDQFMEAITVSAAGDEDEDESG--EERLPSCFDYVMHFLTVFWKVLFACVPP 742
Qу
           Db
        715 LVIGTHSWREOFLEAITVS-AGDEEEEEDGSREERLPSCFDYVMHFLTVFWKVLFACVPP 773
        743 TEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASK 802
Qу
           Db
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    04-JUL-2003 (first entry)
DT
XX
DE
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XX
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    Human; 69039; neuroprotective; gene therapy; haematopoietic disorder;
    Na+/Ca2+ exchanger; ion transporter; neural tissue;
KW
KW
    neurological disorder.
XX
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XX
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XX
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    10-APR-2003.
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    27-SEP-2002; 2002WO-US030817.
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PR
    28-SEP-2001; 2001US-0325737P.
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PA
    (MILL-) MILLENIUM PHARM INC.
XX
PΙ
    Carroll JM;
XX
    WPI; 2003-381617/36.
DR
DR
    N-PSDB; ACC00414.
XX
PT
    Identifying a nucleic acid molecule associated with a disorder for
PT
    preparing a composition for treating hematopoietic or neurological
PT
    disorder by detecting the presence of a nucleic acid molecule in the
    sample that is amplified.
PT
XX
PS
    Example 1; Page 110; 133pp; English.
XX
CC
    The present sequence is the protein sequence for human 69039, a novel
CC
    Na+/Ca2+ exchanger family member (ion transporter). 69039 was shown to be
CC
    expressed in human haematopoietic cells, e.g. CD34-expressing progenitor
CC
    cells as well as in neural tissues, e.g. brain cortex and hypothalamus.
CC
    69039 may therefore be used for preparing a composition for treating
CC
    haematopoietic or neurological disorder
XX
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                     100.0%; Pred. No. 4.9e-294;
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Search completed: June 24, 2004, 16:11:56

Job time: 67.95 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2004, 16:09:57; Search time 23.3089 Seconds

(without alignments)

2039.888 Million cell updates/sec

Title: US-10-054-680-2

Perfect score: 4797

Sequence: 1 MAWLRLQPLTSAFLHFGLVT.....LWLLYILFATLEAYCYIKGF 921

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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1: /cgn2_6/ptodata/2/iaa/5A COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query				
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1	579	12.1	539	4	US-09-701-068-2	Sequence 2, Appli
2	506	10.5	474	4	US-09-701-068-5	Sequence 5, Appli
3	128.5	2.7	693	4	US-09-564-805-234	Sequence 234, App
4	128.5	2.7	4654	3	US-08-476-515A-84	Sequence 84, Appl
5	128.5	2.7	4655	3	US-08-652-877-84	Sequence 84, Appl
6	128.5	2.7	4655	3	US-08-652-877-86	Sequence 86, Appl
7	128.5	2.7	4655	3	US-08-652-877-88	Sequence 88, Appl
8	128.5	2.7	4655	3	US-08-652-877-90	Sequence 90, Appl
9	121	2.5	325	4	US-09-489-039A-13618	Sequence 13618, A
10	116	2.4	355	4	US-09-543-681A-5929	Sequence 5929, Ap
11	115.5	2.4	1786	3	US-08-973-462-8	Sequence 8, Appli

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ALIGNMENTS

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; Sequence 2, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
  APPLICANT: Galil, Gad et al.
  TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
  TITLE OF INVENTION: EXPRESSING SAME
  FILE REFERENCE: 01/21317
  CURRENT APPLICATION NUMBER: US/09/701,068
  CURRENT FILING DATE: 2001-05-07
  NUMBER OF SEQ ID NOS: 17
   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
   LENGTH: 539
;
    TYPE: PRT
   ORGANISM: Arabidopsis thaliana
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Dk)	29	FPGENTLSDGL-RGVLYFLGLAYCFIGLSAITARFFKSMENVVKHSRKVVTIDPITKAEV	87
Q۷	7	124	TTI-RVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	179
Dk)	88	ITYKKVWNFTIADISLLAFGTSFPQISLATIDAIRNMGERY-AGGLGPGTLVGSAAFDLF	146
QΣ	7	180	<pre>IIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLF : </pre>	239
Dk		147	PIHAVCVVVPKAGELKKISDLGVWLVELVWSFWAYIWLYIILEVWSPNVITLVEALLTVL	206
QΣ	?		FFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDG : : :: : : : : : :	
Db)	207	CYGLLLVHAYAQDKRWPYLSLPMSRGDRPE	236
Qζ			NLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQAT	
Dk		237	: : : : EWVPEEIDTSKDDNDND	253
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Dk)	254	: : :: : : VHDVYSDAAQDAV	266
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Dk		267		275
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Dk		307	AK	308
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; Sequence 5, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
  TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEO ID NO 5
  LENGTH: 474
   TYPE: PRT
   ORGANISM: Arabidopsis thaliana
US-09-701-068-5
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Db
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Db
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Db
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US-09-564-805-234
; Sequence 234, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
  TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
  TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
  CURRENT APPLICATION NUMBER: US/09/564,805
  CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
  PRIOR APPLICATION NUMBER: 09/434,382
 PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
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; SEQ ID NO 234
; LENGTH: 693
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TYPE: PRT
  ORGANISM: Arabidopsis thaliana
US-09-564-805-234
                   2.7%; Score 128.5; DB 4; Length 693;
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 Best Local Similarity 19.6%; Pred. No. 0.0031;
 Matches 132; Conservative 88; Mismatches 206; Indels 249; Gaps 32;
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; Patent No. 6239270
  GENERAL INFORMATION:
     APPLICANT: Akerstrom, Goran
    APPLICANT: Juhlin, Claes
    APPLICANT: Rask, Lars
    APPLICANT: Crumley, Gregg R.
    APPLICANT: Morse, Clarence C.
    APPLICANT: Murray, Edward M. APPLICANT: Hjalm, Goran
    TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
    TITLE OF INVENTION: Thereof and DNA Encoding Same
    NUMBER OF SEQUENCES: 84
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Martin Savitzky
      STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
      STREET:
                3C43,
      CITY: Collegeville
      STATE: PA
      COUNTRY: USA
      ZIP: 19426-0107
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: Compaq PC
;
      OPERATING SYSTEM: Windows 95
;
      SOFTWARE: Word 7.0 (Patentin)
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/476,515A
      FILING DATE: 07-JUN-1995
      CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/344,836
      FILING DATE: 23-NOV-1994
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: WO PCT/SE94/00483
      FILING DATE: 24-MAY-1994
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: SE 9301764-8
      FILING DATE: 24-MAY-1993
    ATTORNEY/AGENT INFORMATION:
      NAME: Savitzky, Martin
      REGISTRATION NUMBER: 29,699
      REFERENCE/DOCKET NUMBER: A1355D
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 610-454-3816
      TELEFAX: 610-454-3808
   INFORMATION FOR SEO ID NO:
    SEQUENCE CHARACTERISTICS:
     LENGTH: 4654 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
US-08-476-515A-84
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		Similarity 18.4%; Pred. No. 0.087; 9; Conservative 119; Mismatches 293; Indels 291; Gaps	43;
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Db	1474	: : :: :: :: DSISGRIFWSDATQGKTWSAFQNGTDRRVVFDSSIILTETIAIDWVG	1520
Qу	252	DKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVP	303
Db .	1521	: : : :: : : :: :	1578
Qу	304	LEGKEVDESRREMIK	321
Db	1579	: : : : : : : : : :	1638
Qу	322	DLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKAS	381
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Qу	382	SMSEVHTDEPEDFISKVFFDPCSYQCLENC-	411
Db	1682	:: : :: :	1741
Qу	412	GAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGE	459
Db	1742	: ::: : :	1800
Qу	460	TQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPC	517
Db	1801	: : : : : IHRVKTDGTNRTVFASISMVGPSMNLA	1827
Qу	518	VATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAK	574
Db	1828	:: : : : : LDWISRNLYSTNPRTQSIEVLTLHGDIRYRKTLIANDGTAL	1868
Qу	575	GGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEY	608
Db	1869	: : :: :: ::: :::::::::::::::::::	1928
QУ	609	ERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKP-VLGEHPKLEVIIEES	667
Db	1929	EEQKLYWAVTGRGV-IERGNVDGTDRMILVHQLSHPWGIAVHDSFLYYTDEQ	1979
Qу	668	YEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYV	725
Db	1980	YEVIERVDKATGANKIVLRDNVPNLRGLQVYHRRNAAESSNGCSNNM	2026
Qу	726	MHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLAS :	771
Db	2027	NACQQICLPVPGGLFSCACATGFKLNPDNRSCSPYNSFIVVSMLSAIRGFSLELSD	2082
Qу	772	HFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYAD-ASIGNVT	819

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Db
        2143 GENGVR---GIAVDWVAGNLYF 2161
RESULT 5
US-08-652-877-84
; Sequence 84, Application US/08652877
; Patent No. 6187548
  GENERAL INFORMATION:
    APPLICANT: Akerstrom, Goran
;
    APPLICANT: Juhlin, Claes
    APPLICANT: Rask, Lars
    APPLICANT: Crumley, Gregg R.
    APPLICANT: Morse, Clarence C.
    APPLICANT: Murray, Edward M.
    APPLICANT: Hjalm, Goran
    TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
    TITLE OF INVENTION: Thereof and DNA Encoding Same
   NUMBER OF SEQUENCES: 106
    CORRESPONDENCE ADDRESS:
     ADDRESSEE: Rhone-Poulenc Rorer Inc.
      STREET: 500 Arcola Rd., 3C43
      CITY: Collegeville
      STATE: PA
      COUNTRY: USA
;
      ZIP: 19426-0107
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: Macintosh
      OPERATING SYSTEM: System 7.5.1
      SOFTWARE: Word 6.0 (Patentin)
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/652,877
      FILING DATE:
      CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: PCT/US95/15203
      FILING DATE: 22-NOV-1995
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/344,836
      FILING DATE: 23-NOV-1994
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/487,314
      FILING DATE: 07-JUNE-1995
    ATTORNEY/AGENT INFORMATION:
      NAME: Savitzky, Martin
      REGISTRATION NUMBER: 29,699
      REFERENCE/DOCKET NUMBER: A1355E-US
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 610-454-3816
      TELEFAX: 610-454-3808
  INFORMATION FOR SEQ ID NO: 84:
   SEQUENCE CHARACTERISTICS:
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LENGTH: 4655 amino acids

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;
     TYPE: amino acid
     TOPOLOGY: linear
   MOLECULE TYPE: protein
US-08-652-877-84
                  2.7%; Score 128.5; DB 3; Length 4655;
 Query Match
 Best Local Similarity 18.4%; Pred. No. 0.087;
 Matches 159; Conservative 119; Mismatches 293; Indels 291; Gaps 43;
       156 CGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHL----- 200
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          Db
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                                1:1
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Qу
                  1639 DLIIRHP-----YALTLFEDS-VYWTDRATRRVMRAN---KWHGGNQSVVMY 1681
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       382 SMS-----EVHTDEPEDFISKVFFDPCSYOC-------LENC- 411
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                1682 NIQWPLGIVAVHPSKQPNSVNPCAFSRCSHLCLLSSQGPHFYSCVCPSGWSLSPDLLNCL 1741
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Qу
       412 --GAVLLTVVRKGGDMSKTMYVDYKTED-----GSANAGADYEFTEGTV----VLKPGE 459
              Db
      1742 RDDQPFLITVRQHIIFGISLNPEVKSNDAMVPIAGIQN-GLDVEFDDAEQYIYWVENPGE 1800
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                      :| :| !: : | ||
      Db
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       668 YEFKTTVDKLIKKTNLALVVGTHSWRDQF--MEAITVSAAGDEDEDESGEERLPSCFDYV 725
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Db
        2143 GENGVR---GIAVDWVAGNLYF 2161
RESULT 6
US-08-652-877-86
; Sequence 86, Application US/08652877
; Patent No. 6187548
  GENERAL INFORMATION:
    APPLICANT: Akerstrom, Goran
    APPLICANT: Juhlin, Claes
    APPLICANT: Rask, Lars
    APPLICANT: Crumley, Gregg R.
    APPLICANT: Morse, Clarence C.
    APPLICANT: Murray, Edward M.
    APPLICANT: Hjalm, Goran
    TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
    TITLE OF INVENTION: Thereof and DNA Encoding Same
    NUMBER OF SEQUENCES: 106
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Rhone-Poulenc Rorer Inc.
      STREET: 500 Arcola Rd., 3C43
      CITY: Collegeville STATE: PA
      COUNTRY: USA
      ZIP: 19426-0107
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: Macintosh
      OPERATING SYSTEM: System 7.5.1
      SOFTWARE: Word 6.0 (Patentin)
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/652,877
      FILING DATE:
      CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: PCT/US95/15203
      FILING DATE: 22-NOV-1995
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/344,836
      FILING DATE: 23-NOV-1994
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/487,314
      FILING DATE: 07-JUNE-1995
    ATTORNEY/AGENT INFORMATION:
      NAME: Savitzky, Martin
      REGISTRATION NUMBER: 29,699
      REFERENCE/DOCKET NUMBER: A1355E-US
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TELECOMMUNICATION INFORMATION:
     TELEPHONE: 610-454-3816
     TELEFAX: 610-454-3808
 INFORMATION FOR SEQ ID NO: 86:
   SEQUENCE CHARACTERISTICS:
    LENGTH: 4655 amino acids
     TYPE: amino acid
     TOPOLOGY: linear
   MOLECULE TYPE: protein
US-08-652-877-86
 Query Match 2.7%; Score 128.5; DB 3; Length 4655; Best Local Similarity 18.4%; Pred. No. 0.087;
 Matches 159; Conservative 119; Mismatches 293; Indels 291; Gaps 43;
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           Db
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               Db
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          1869 GVGFPIGITVDPARGKLYWSDQGTDSGVPAKIASANMDGTSVKTLFTGNLEHLECVTLDI 1928
       609 EROENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKP-VLGEHPKLEVIIEES 667
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        1980 YEVIERVDKATGANKIVL-----RDNVPNLRGLQVYHRRNAAESSNG----CSNNM 2026
         726 MHFLTVFWKV---LFACV-----PPTEYCHGWACFAVSILIIGMLTAIIG---DLAS 771
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        2027 NACQQICLPVPGGLFSCACATGFKLNPDNRSCSPYNSF----IVVSMLSAIRGFSLELSD 2082
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Dh
RESULT 7
US-08-652-877-88
; Sequence 88, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
    APPLICANT: Akerstrom, Goran
    APPLICANT: Juhlin, Claes
APPLICANT: Rask, Lars
;
    APPLICANT: Crumley, Gregg R.
    APPLICANT: Morse, Clarence C.
    APPLICANT: Murray, Edward M.
    APPLICANT: Hjalm, Goran
    TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
    TITLE OF INVENTION: Thereof and DNA Encoding Same
    NUMBER OF SEQUENCES: 106
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Rhone-Poulenc Rorer Inc.
      STREET: 500 Arcola Rd., 3C43
      CITY: Collegeville
      STATE: PA
      COUNTRY: USA
      ZIP: 19426-0107
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: Macintosh
      OPERATING SYSTEM: System 7.5.1
      SOFTWARE: Word 6.0 (Patentin)
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/652,877
      FILING DATE:
      CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: PCT/US95/15203
      FILING DATE: 22-NOV-1995
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/344,836
      FILING DATE: 23-NOV-1994
    PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/487,314
     FILING DATE: 07-JUNE-1995
   ATTORNEY/AGENT INFORMATION:
     NAME: Savitzky, Martin
     REGISTRATION NUMBER: 29,699
     REFERENCE/DOCKET NUMBER: A1355E-US
   TELECOMMUNICATION INFORMATION:
     TELEPHONE: 610-454-3816
     TELEFAX: 610-454-3808
  INFORMATION FOR SEQ ID NO: 88:
   SEQUENCE CHARACTERISTICS:
    LENGTH: 4655 amino acids
     TYPE: amino acid
     TOPOLOGY: linear
   MOLECULE TYPE: protein
US-08-652-877-88
                   2.7%; Score 128.5; DB 3; Length 4655;
 Query Match
 Best Local Similarity 18.4%; Pred. No. 0.087;
 Matches 159; Conservative 119; Mismatches 293; Indels 291; Gaps 43;
       156 CGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHL----- 200
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          1639 DLIIRHP-----YALTLFEDS-VYWTDRATRRVMRAN---KWHGGNOSVVMY 1681
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              Db
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               2083 HSETMVPVAGQGRNALHVDVDVSSGFIYWCDFSSSVASDNAIRRIKPDGSSLMNIVTHGI 2142
Db
Qy
        820 GSNAVNVFLGIGLAWSVAAIYW 841
            Db
       2143 GENGVR---GIAVDWVAGNLYF 2161
RESULT 8
US-08-652-877-90
; Sequence 90, Application US/08652877
; Patent No. 6187548
  GENERAL INFORMATION:
    APPLICANT: Akerstrom, Goran
    APPLICANT: Juhlin, Claes
APPLICANT: Rask, Lars
    APPLICANT: Crumley, Gregg R.
    APPLICANT: Morse, Clarence C.
    APPLICANT: Murray, Edward M.
    APPLICANT: Hjalm, Goran
    TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
    TITLE OF INVENTION: Thereof and DNA Encoding Same
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     ADDRESSEE: Rhone-Poulenc Rorer Inc.
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     CITY: Collegeville
      STATE: PA
     COUNTRY: USA
      ZIP: 19426-0107
    COMPUTER READABLE FORM:
     MEDIUM TYPE: Floppy disk
     COMPUTER: Macintosh
      OPERATING SYSTEM: System 7.5.1
      SOFTWARE: Word 6.0 (Patentin)
    CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/08/652,877
     FILING DATE:
     CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PCT/US95/15203
     FILING DATE: 22-NOV-1995
    PRIOR APPLICATION DATA:
     APPLICATION NUMBER: US 08/344,836
     FILING DATE: 23-NOV-1994
    PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/487,314
     FILING DATE: 07-JUNE-1995
    ATTORNEY/AGENT INFORMATION:
     NAME: Savitzky, Martin
     REGISTRATION NUMBER: 29,699
     REFERENCE/DOCKET NUMBER: A1355E-US
    TELECOMMUNICATION INFORMATION:
     TELEPHONE: 610-454-3816
     TELEFAX: 610-454-3808
  INFORMATION FOR SEQ ID NO: 90:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 4655 amino acids
     TYPE: amino acid
     TOPOLOGY: linear
    MOLECULE TYPE: protein
US-08-652-877-90
 Query Match 2.7%; Score 128.5; DB 3; Length 4655; Best Local Similarity 18.4%; Pred. No. 0.087;
 Matches 159; Conservative 119; Mismatches 293; Indels 291; Gaps 43;
Qу
       156 CGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHL----- 200
           1415 CDTGYMLESDGRTCKV-TASESLLLLVASQNKIIADSVTSQVHNIYSLVENGSYIVAVDF 1473
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Db
       1474 DSISGRIFWSDATQGKTWSAFONGTDRRV--VFDSSII-----LTETIAIDWVG 1520
       252 DKRLLFYKYMHKKYRTDK----HRGIIIETEGDHPKGIEMDGKMMNSHFLD----GNLVP 303
Qу
            1521 -RNLYWTDYALETIEVSKIDGSHRTVLISKNLTNPRGLALDPR-MNEHLLFWSDWGHHPR 1578
        304 LEGKEVDESRREMI-----K 321
Qу
           :| :| 1 | :|
Db
       1579 IERASMDGSMRTVIVQDKIFWPCGLTIDYPNRLLYFMDSYLDYMDFCDYNGHHRRQVIAS 1638
        322 DLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKAS 381
Qv
           Db
       1639 DLIIRHP-----YALTLFEDS-VYWTDRATRRVMRAN---KWHGGNQSVVMY 1681
Qy
        382 SMS-----EVHTDEPEDFISKVFFDPCSYQC-------LENC- 411
           :: | | | | | | | |
       1682 NIQWPLGIVAVHPSKQPNSVNPCAFSRCSHLCLLSSQGPHFYSCVCPSGWSLSPDLLNCL 1741
Db
Qу
       412 --GAVLLTVVRKGGDMSKTMYVDYKTED-----GSANAGADYEFTEGTV----VLKPGE 459
                1742 RDDQPFLITVRQHIIFGISLNPEVKSNDAMVPIAGION-GLDVEFDDAEQYIYWVENPGE 1800
Db
       460 TOKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEOPEEGMPPAIFNSLPL--PRAVLASPC 517
Qу
                                         :| :| !: ! | | |
```

```
Db
       1801 IHR------VKTDGTNRTVFASISMVGPSMNLA--- 1827
        518 VATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSG---ARGTVIVPFRTVEGTAK 574
Qу
            1828 -----LDWISRNLY-----STNPRTQSIEVLTLHGDIRYRKTLIAN----DGTAL 1868
Db
        575 GGGEDF----EDTYGELEFKNDETVKTIRVKIVDEE-----EY 608
Qу
           1869 GVGFPIGITVDPARGKLYWSDQGTDSGVPAKIASANMDGTSVKTLFTGNLEHLECVTLDI 1928
Db
Qy
        609 ERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKP-VLGEHPKLEVIIEES 667
           Db
       1929 EEQKLYWAVTGRGV-IERGNVDGTDRMIL-----VHQLSHPWGIAVHDSFLYYTDEQ 1979
       668 YEFKTTVDKLIKKTNLALVVGTHSWRDQF--MEAITVSAAGDEDEDESGEERLPSCFDYV 725
Qy
               Db
       1980 YEVIERVDKATGANKIVL-----RDNVPNLRGLQVYHRRNAAESSNG-----CSNNM 2026
       726 MHFLTVFWKV---LFACV------PPTEYCHGWACFAVSILIIGMLTAIIG---DLAS 771
Qу
               2027 NACQQICLPVPGGLFSCACATGFKLNPDNRSCSPYNSF----IVVSMLSAIRGFSLELSD 2082
Db
       772 HFGCTIGL----KDSVTAVVFVAFGTSVPDTFASKAA---ALQDVYAD-ASIGNVT---- 819
Qу
           2083 HSETMVPVAGQGRNALHVDVDVSSGFIYWCDFSSSVASDNAIRRIKPDGSSLMNIVTHGI 2142
Qу
       820 GSNAVNVFLGIGLAWSVAAIYW 841
           | | | | | | | | | | | |
       2143 GENGVR---GIAVDWVAGNLYF 2161
RESULT 9
US-09-489-039A-13618
; Sequence 13618, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13618
  LENGTH: 325
  TYPE: PRT
  ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13618
 Query Match
                     2.5%; Score 121; DB 4; Length 325;
 Best Local Similarity 28.9%; Pred. No. 0.0045;
 Matches 46; Conservative 24; Mismatches 59; Indels 30; Gaps 7;
Qy 754 VSILIIGMLTAIIGD----LASHFG---CTIGLKDSVTAVVFVAFGTSVPDTFASKAAAL 806
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181 VAMIVMPMATRMVVDNSTVLANYFAISELTVGL-----TVVAIGTSLPE-LATAIAGA 232
Db
        807 QDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFT--I 864
Qy
                1:|||:|:|:|:|:|:|:|:|
Db
        233 RKGEDDIAIGNIIGANILNIALVLGLPALIAP-----GSFATEAFTRDYGVMLLVSLI 285
        865 FAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLW 903
Qy
           Db
        286 FAVLC-----WRRQQQPGRLVGALLVGGFVVWLAMLFW 318
RESULT 10
US-09-543-681A-5929
; Sequence 5929, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS
MIRABILIS FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEO ID NOS: 8344
; SEO ID NO 5929
 LENGTH: 355
   TYPE: PRT
  ORGANISM: Proteus mirabilis
US-09-543-681A-5929
 Query Match 2.4%; Score 116; DB 4; Length 355; Best Local Similarity 25.1%; Pred. No. 0.016;
 Matches 45; Conservative 30; Mismatches 70; Indels 34; Gaps
        745 YCHGW----ACFAVSILIIGMLTAIIGD----LASHFGCTIGLKDSVTAVVFVAFGTSV 795
Qу
           21 FTHCWKTDGMLITLSLLIVGLMLLVYASDRLVYGASVFAQSLKLPPAVIGIVIVGMGTSL 80
Qу
        796 PDTFASKAAALQDVYADASIGNVTGSNAVNVFL--GIGLAWSVAAIYWALQGQEFHVSAG 853
           Db
        81 PELFVATDAAIHNL-PEIAIGTAIGSSLTNLLLIAGIG----AMIY-----PMNIQSA 128
        854 TLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATL 912
Qу
            129 VLKKELPLMII-----VILLAGLVVSNSHLGLREGCLL----FFIGFASLFLMIKML 176
RESULT 11
US-08-973-462-8
; Sequence 8, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE
```

```
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
  FILE REFERENCE: 0660-0125-0 PCT
  CURRENT APPLICATION NUMBER: US/08/973,462B
  CURRENT FILING DATE: 1998-02-06
  EARLIER APPLICATION NUMBER: PCT/FR96/00894
  EARLIER FILING DATE: 1996-06-12
; EARLIER APPLICATION NUMBER: FR 95/07007
; EARLIER FILING DATE: 1995-06-13
; NUMBER OF SEO ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
  LENGTH: 1786
   TYPE: PRT
  ORGANISM: Artificial Sequence
  OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-08-973-462-8
 Query Match 2.4%; Score 115.5; DB 3; Length 1786; Best Local Similarity 20.5%; Pred. No. 0.31;
 Matches 94; Conservative 79; Mismatches 168; Indels 117; Gaps 22;
       268 DKHRGIIIE--TEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRREMIRILKDLKQ 325
           1197 EKDVSLVVEEVQDNDMDESVE---KVLELKNMEEELMK-DAVEINDITSKLIEETOELNE 1252
        326 KHPE--KDLDOLVEMANYYALSHOOKSRAFYRIOATRMMTGAGNILKKHAAEOAKKASSM 383
Qy
              Db
       1253 VEADLIKDMEKLKELEK--ALSEDSK-----EIIDAKDDTLEKVIEEEHDITTTL 1300
        384 SEV--HTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSAN 441
Qу
            1301 DEVVELKDVEEDKIEKV------SDLKDLEEDILKEVKEIKELESEILEDYKE----- 1347
Db
       442 AGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEOPEEGMPPA 501
Qу
                     1348 ------LKTIETD-----ILEEKKEIEKDHF-----EKFEEEAEE----- 1376
Dh
Qу
       502 IFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGT 561
                            : | | | :: | | : | | ::
       1377 -----IKDLEADILK-EVSSLEVEEEKKLEEVHELKEEVEH-- 1411
Dh
        562 VIVPFRTVEGTAKGGGEDFEDTYGEL--EFKNDETVKTIRVKIVDEEEYERQENFFIALG 619
Qу
                ::| : |::| |: ||
Db
       1412 IISGDAHIKGLEEDDLEEVDDLKGSILDMLKGD-----MELGDMDK-ESLEDVTTKLG 1463
       620 EPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL-EVIIEESYEFKTTVDKLI 678
Qу
           1464 E---RVESLKDVLSSALGMDEEQMKTRKK-----AQRPKLEEVLLKE--EVKEEPKKKI 1512
Db
       679 KKTNLALVVGTHSWRDOFMEAITVSAAGDEDEDESGEE 716
Qγ
            1 : : : !: : ! !! !!
       1513 TKKKVRFDIKDKEPKDEIVEV----EMKDEDIEEDVEE 1546
Db
```

```
; Sequence 2, Application US/07853913
; Patent No. 5338839
  GENERAL INFORMATION:
    APPLICANT: McKay, Ronald D.G.
    APPLICANT: Lendahl, Urban
    TITLE OF INVENTION: Nestin Expression As An Indicator of
    TITLE OF INVENTION: Neuroepithelial Tumors
    NUMBER OF SEQUENCES: 4
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
      STREET: Two Militia Drive
;
      CITY: Lexington
      STATE: Massachusetts
      COUNTRY: U.S.A.
      ZIP: 02173
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/07/853,913
      FILING DATE: 19920319
      CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/660,412
;
      FILING DATE: 22-FEB-1991
;
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/603,803
      FILING DATE: 25-OCT-1990
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/201,762
      FILING DATE: 02-JUN-1988
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/180,548
    ATTORNEY/AGENT INFORMATION:
      NAME: Granahan, Patricia
      REGISTRATION NUMBER: 32,227
      REFERENCE/DOCKET NUMBER: MIT-4641AAAA
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 617-861-6240
      TELEFAX: 617-861-9540
  INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1805 amino acids
      TYPE: AMINO ACID
      TOPOLOGY: linear
    MOLECULE TYPE: protein
US-07-853-913-2
 Query Match
                         2.4%; Score 115.5; DB 1; Length 1805;
 Best Local Similarity 18.8%; Pred. No. 0.32;
         99; Conservative 89; Mismatches 215; Indels 123; Gaps
         268 DKHRGIIIETEGDHPKGI-EMDGKMMNSHFLDGNLVPLEGKEVDESRREMIRILKDLKQK 326
Qу
             1: | :: | | | | :: |:
                                             734 DQEAGRSLQKENQEPLGYEEAEDQMLE-----RLIEKESQESLKSPEENQRIGKPLERE 787
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```
327 HPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEV 386
Qy
           ::|| | | | ::: : |:|
Db
        788 N-QKSLRYLEENQETFVPLESRNQRP---LRSLEVEEEEQRIVKPLEKVSQDSLGSLAEE 843
        387 HTD----EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSAN 441
Qу
                 Db
        844 NVOPLRYLEEDDCINKSLLEDKTHKSLGS------LEDRNGD 879
        442 AGADYEFTEGTVVLKPGETQKEFSVGIIDDD-----IFEEDEHFFVR-----LSN 486
Qy
           880 SIIIPQESETQVSLRPPEEEDQRIVNHLEKESQEFSRSSEEEEQVMERSLEGENHESLSS 939
Db
        487 VRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIF-----TFE 535
Qу
           | |:: | : :| | | | |:::|
        940 VEKEDQMVESQLEKESQDS----GKSLEDESQETFGPLEKENAESLRSLAGQDQEEQKLE 995
Db
        536 CDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
Qу
           :| ::| :: | : |: |: |: |: ||
        996 QETQQTLRAVGNEQMAVSPPEKVDPELPKPLGNDQEIARSLGKENQESLVSLKEKGIETV 1055
Db
        596 KTIRVKIVD-----EEEYERQENFFIALGEPKWMER-----GISDVTD 633
Qy
           1 1
       1056 KSLETEIIEPLETAEEDLERRKS--IDTOEPLWSTEVARETVEPPEDEPPGSLGSVDENR 1113
Db
       634 RKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIK-----KTNL 683
Qy
             Db
       1114 ETLTSLEKESQELSSLGK-----WNVETRVEDSQQCLQVEEGLQEEQHQESLREVKQEL 1167
       684 ALVVGTHSWRDQF-----MEA-ITVSAAGDEDEDE-----SGEE 716
Qу
                  Db
       1168 PSSGNQQRWEDVVEGKAVGQEAPLATTGVGTEDKAELHLRGQGGEE 1213
RESULT 13
US-09-134-001C-3608
; Sequence 3608, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3608
  LENGTH: 339
   TYPE: PRT
  ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3608
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Query Match
                      2.4%; Score 113.5; DB 4; Length 339;
 Best Local Similarity 20.4%; Pred. No. 0.026;
 Matches 69; Conservative 53; Mismatches 149; Indels 67; Gaps 12;
        195 RKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKR 254
Qy
            3 RKIKRSDLMF-SIGFIIIAVIIVVALLILFSFVPVGLWISALAA---GVHVGIGTLVGMR 58
Db
        255 LLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFL-----DGNL--- 301
Qу
           1 1:
         59 L----RRVSPRKVIAPLIKAHKAGLNLTTNQLESHYLAGGNVDRVVDANIAAQR 108
Db
        302 ----VPLE-GKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRI 356
Qу
               :| | | :|:: |::: _ ;|: _ ;|:
                                                 : : |:| |
Db
        109 ADIDLPFERGAAIDLAGRDVLEAVQ--MSVNPKVIETPFIAGVAMNGIEVKAKARITVRA 166
        357 QATRMMTGAG-NILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVL 415
Qу
               |:: ||| : | | || ||
        167 NIARLVGGAGEETIIARVGEGIVSTIGSSEHHT-----EVLENPDNIS 209
Db
        416 LTVVRKG---GDMSKTMYVDYKTEDGSANAGADYE----FTEGTVVLKPGETQKEFSVGI 468
Qу
             ||:|| | :::| | | | | | | : : : | ::: :|
        210 KTVLSKGLDSGTAFEILSIDIADVDISKNIGADLQTEQALADKNIAQAKAEERRAMAVA- 268
Db
        469 IDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSL 506
Qy
                 Db
        269 -----SEQEMKARVQEMRAKVVEAESEVPLAMAEAL 299
RESULT 14
US-09-134-001C-3350
; Sequence 3350, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
  CURRENT FILING DATE: 1998-08-13
  PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3350
  LENGTH: 660
   TYPE: PRT
  ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3350
 Query Match
                      2.3%; Score 111; DB 4; Length 660;
 Best Local Similarity 19.1%; Pred. No. 0.15;
 Matches 83; Conservative 67; Mismatches 131; Indels 154; Gaps
Qy 556 SGARGTVIVPFRTVEG-----TAKGGGEDFE-----DTYGE 586
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1 | | :: ::|
                                           Db
         30 STVAGDVIARYKRMQGYDVRYLTGTDEHGQKIQEKAQKAGKTELEYLDEMISGIKNLWSK 89
Qу
        587 LEFKNDETVKTI--RVKIVDEEEYER-QENFFIALGEPKWMERGISDVTDRKLTMEEEEA 643
            Db
         90 LEISNDDFIRTTEERHKQVVEKVFERLLKQGDIYLGE----YEGWYSVPDETYYTESOLV 145
        644 KRIAEMGKPVLGEHP----KLEVIIEESYEFKTT--VDKLIK----- 679
Qy
             146 DPVYENGKIVGGKSPDSGHEVELVKEESYFFNINKYTDRLLEFYDENPDFIQPPSRKNEM 205
Db
Qу
        680 -----KTNLALVVGTHSWRDQ------FMEAIT--VSAAGDEDEDES---- 713
                    :||: : | : :::|: :|: :|::
Db
        206 INNFIKPGLEDLAVSRTSFDWGVRVPSNPKHVVYVWIDALVNYISSLGYLSDDETLFNKY 265
        714 -----GEERLPSCFDYVMHFLTVFWKVLFAC----VPPTEYCHGWACFAVSILIIGM 761
Qу
                  :| :: | :: | :| :| :| |
Db
        266 WPADIHLMAKE-----IVRFHSIIWPILLMALDLPLPKKVFAHGWI----LMKDGK 312
        762 LTAIIGD-----LASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASI 815
Qу
           Db
        313 MSKSKGNVVDPNVLIDRYGLDATRYYLMRELPFGSDGVFTPEAFVER----TNYDL 364
Qy
        816 GNVTGSNAVNVFLGIGLAWSVAAIYW-----ALQG-------QEFHVSAG 853
            365 ANDLG-NLVNRTI-----SMINKYFHGELPAYQGPKHELDEKMEAMALETVKSFNDNME 417
Qy
       854 TLAFSVTLFTIFAFV 868
           : | | | | | | | : : | :
        418 SLQFSVALSTVWKFI 432
RESULT 15
US-09-134-001C-3159
; Sequence 3159, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
  FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3159
  LENGTH: 10182
   TYPE: PRT
  ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3159
 Query Match
                     2.3%; Score 111; DB 4; Length 10182;
 Best Local Similarity 21.2%; Pred. No. 18;
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Matche	es 9'	7; Conservative 70; Mismatches 168; Indels 122; Gaps 22;	;
Qy	310	DESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQK 349	
Db	9479	DATSNDLVNQAKDEGQSAIEHIHADELPKAKLDANQMIDQKVEDINHLISQNPNLSNEEK 9538	}
Qy	350	SRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSY 405 :: : ::: : : : : : : : : : :	
Db	9539	NKLISQINKLVNGIKNEIQQAINKQQIENATTKLDEVIETTKKLIIAKAEAK 9590)
Qy	406	QCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFS 465	
Db	9591	QMIKELSQKKRDAINNNTDLTPSQKAHALADIDKTEKDALQHIENS 9636	;
Qy	466	VGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVA 519	
Db	9637	NSIDDINNNKEHAFNTLAHIIIWDTDQQPLVFEVPELSLQNALVTSEVVVHRDE 9690)
Qy	520	TVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVE 570	
Db	9691	TISLESIKKKMTLTDELKVNIVSLP-NTDKVADHL-TAKVKVILADGSYVTVNVPVKVVE 9748	}
Qy	571	GTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQ 611	
Db	9749	KELQIAKKDAIKTIDVLVKQKIKDIDSNNELTSTQREDAKAEIERL 9794	ſ
Qу	612	ENFFIALGEPKWMERGISDVTDRKLTMEEEEAKR-IAEMGKPVLGEH 657 : : : : : :	
Db	9795	KKQAIDKVNHSKSIKDIETVKRTDFEEIDQFDPKRFTLNKAKKDIITDVNTQIQNGF 9851	-
Qу	658	PKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHS 691 :: : :: :	
Db	9852	KEIETIKGLTSNEKTQFDKQLTALQKEFLEKVEHAHN 9888	

Search completed: June 24, 2004, 16:15:52 Job time: 26.3089 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2004, 16:07:32; Search time 20.9182 Seconds

(without alignments)

4235.175 Million cell updates/sec

Title: US-10-054-680-2

Perfect score: 4797

Sequence: 1 MAWLRLQPLTSAFLHFGLVT.....LWLLYILFATLEAYCYIKGF 921

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ક				
sult		Query				
No.	Score	Match	Length	DB	ID	Description
1	3447.5	71.9	970	2	A36417	Na+/Ca2+-exchangin
2	3441	71.7	935	2	S43730	Na+/Ca2+-exchangin
3	3439.5	71.7	973	2	S32815	Na+/Ca2+-exchangin
4	3437.5	71.7	941	2	B53335	Na+/Ca2+-exchangin
5	3434.5	71.6	958	2	S32435	Na+/Ca2+-exchangin
6	3432.5	71.6	970	2	I48097	Na+/Ca2+-exchangin
7	3426	71.4	957	2	A53789	Na+/Ca2+-exchangin
8	3425.5	71.4	970	2	S27114	Na+/Ca2+-exchangin
9	3422	71.3	971	2	S28833	Na+/Ca2+-exchangin
10	3357	70.0	921	2	A54139	Na+/Ca2+-exchangin
11	2007	41.8	890	2	B89047	protein C10G8.5 [i
12	1192	24.8	807	2	T24110	hypothetical prote
13	659	13.7	152	2	152640	cardiac sodium/cal
	No. 1 2 3 4 5 6 7 8 9 10 11 12	No. Score 1 3447.5 2 3441 3 3439.5 4 3437.5 5 3434.5 6 3432.5 7 3426 8 3425.5 9 3422 10 3357 11 2007 12 1192	No. Score Match 1 3447.5 71.9 2 3441 71.7 3 3439.5 71.7 4 3437.5 71.7 5 3434.5 71.6 6 3432.5 71.6 7 3426 71.4 8 3425.5 71.4 9 3422 71.3 10 3357 70.0 11 2007 41.8 1192 24.8	No. Score Match Length 1 3447.5 71.9 970 2 3441 71.7 935 3 3439.5 71.7 973 4 3437.5 71.7 941 5 3434.5 71.6 958 6 3432.5 71.6 970 7 3426 71.4 957 8 3425.5 71.4 970 9 3422 71.3 971 10 3357 70.0 921 11 2007 41.8 890 12 1192 24.8 807	No. Score Match Length DB 1 3447.5 71.9 970 2 2 3441 71.7 935 2 3 3439.5 71.7 973 2 4 3437.5 71.7 941 2 5 3434.5 71.6 958 2 6 3432.5 71.6 970 2 7 3426 71.4 957 2 8 3425.5 71.4 970 2 9 3422 71.3 971 2 10 3357 70.0 921 2 11 2007 41.8 890 2 12 1192 24.8 807 2	No. Score Match Length DB ID 1 3447.5 71.9 970 2 A36417 2 3441 71.7 935 2 S43730 3 3439.5 71.7 973 2 S32815 4 3437.5 71.7 941 2 B53335 5 3434.5 71.6 958 2 S32435 6 3432.5 71.6 970 2 I48097 7 3426 71.4 957 2 A53789 8 3425.5 71.4 970 2 S27114 9 3422 71.3 971 2 S28833 10 3357 70.0 921 2 A54139 11 2007 41.8 890 2 B89047 12 1192 24.8 807 2 T24110

14	573.5	12.0	538	2	T00424	probable Na+/Ca2+
15	573	11.9	133	2	A48852	Na+/Ca2+-exchangin
16	312	6.5	1199	2	s20969	Na+/Ca2+,K+-exchan
17	284.5	5.9	1014	2	T31433	Na+/Ca2+,K+-exchan
18	225	4.7	123	2	146959	Na/Ca exchanger NA
19	215.5	4.5	591	2	T19746	hypothetical prote
20	205.5	4.3	1568	2	T08616	aggregation factor
21	201	4.2	4936	2	AH2515	hypothetical prote
22	190.5	4.0	2205	2	T08615	aggregation factor
23	170.5	3.6	611	2	T21747	hypothetical prote
24	169.5	3.5	3016	2	s77300	hypothetical prote
25	161	3.4	825	2	T08617	aggregation factor
26	150.5	3.1	591	2	S40705	Na+/Ca2+,K+-exchan
27	147	3.1	590	2.	S40707	hypothetical prote
28	144.5	3.0	703	2	T03888	Na+/Ca2+,K+-exchan
29	144	3.0	644	2	B96582	hypothetical prote
30	144	3.0	1428	2	AC2224	hypothetical prote
31	143.5	3.0	325	2	F65110	hypothetical 34.7
32	143	3.0	123	2	A53335	Na+/Ca2+-exchangin
33	142.5	3.0	325	2	C91138	hypothetical prote
34	142.5	3.0	325	2	F85983	hypothetical prote
35	142.5	3.0	1807	2	JC6319	· integrin beta-4 ch
36	142	3.0	302	2	C64311	Na+/Ca2+-exchangin
37	141.5	2.9	318	2	G84196	cation antiporter
38	139.5	2.9	826	2	AB1841	hypothetical prote
39	139.5	2.9	1748	1	JN0786	integrin beta-4 ch
40	138	2.9	743	2	Т38674	probable membrane
41	135.5	2.8	325	2	AI0904	probable membrane
42	134	2.8	433	2	S74922	hypothetical prote
43	132	2.8	720	2	T02457	hypothetical prote
44	129.5	2.7	309	2	B72342	conserved hypothet
45	128.5	2.7	664	2	S66067	methionine-tRNA li

ALIGNMENTS

```
RESULT 1
A36417
Na+/Ca2+-exchanging protein - dog
C; Species: Canis lupus familiaris (dog)
C; Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 18-Aug-2000
C; Accession: A36417
R; Nicoll, D.A.; Longoni, S.; Philipson, K.D.
Science 250, 562-565, 1990
A; Title: Molecular cloning and functional expression of the cardiac sarcolemmal Na(+)-Ca(2+) exchanger.
A; Reference number: A36417; MUID:91047958; PMID:1700476
A; Accession: A36417
A; Status: preliminary
A; Molecule type: mRNA
```

A;Cross-references: GB:M57523; NID:g164072; PIDN:AAA62766.1; PID:g164073;

GB:M36119 C;Superfamily: human Na+/Ca2+-exchanging protein C;Keywords: phosphoprotein; transmembrane protein

A; Residues: 1-970 <NIC>

Query Match 71.9%; Score 3447.5; DB 2; Length 970; Best Local Similarity 69.2%; Pred. No. 1e-223; Matches 677; Conservative 109; Mismatches 127; Indels 65; Gaps 10; 1 MAWLRLQPLTSAFLHFGLVTFVLF--LNGLRAEAGGSGDVPSTGONNESCSGSSDCKEGV 58 Qу 1 :11 :: : 11 1: 11: - 1 1 MLQLRLLPTFSMGCHLLAVVALLFSHVDLISAETEMEGEGNETGE----CTGSYYCKKGV 56 Db 59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPN 118 Qу 57 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSOEKEITIKKPN 116 Db 119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM 178 Qy 117 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 176 Db 179 FIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL 238 Qу 177 FIIIALCYYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF 236 Db 239 FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH 295 Qу 237 FFFPICVVFAWVADRRLLFYKYVYKRYRAGKQRGMIIEHEGDRPSSKTEIEMDGKVVNSH 296 Db 296 ---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 348 Qy 1111 11 11 1 1 297 VDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355 Db 349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407 Qу 356 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTYQC 415 Db 408 LENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467 Qу 416 LENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475 Db 468 IIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527 Qy -476 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---ALACLGSPSTATVTIFDDD 532 Db 528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587 Qy 533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592 Db 588 EFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG----- 627 Qy 593 EFONDEIVKTISVKVIDDEEYEKNKTFFLEIGEPRLVEMSEKKALLLNELGGFTITGKYL 652 Db

Qу

Db

Qy

Db

Qу

-----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGEHPKLEVI 663

653 YGQPVFRKVHAREHPIPSTVITIAEEYDDKQPLTSKEEEERRIAEMGRPILGEHTKLEVI 712

724 YVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSV 783

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.773 YVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMIGILTAFIGDLASHFGCTIGLKDSV 832
Db
        784 TAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWAL 843
Qy
           833 TAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAA 892
Db
        844 QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLW 903
Qу
            Db
        893 NGEQFKVSPGTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSCLFVLLW 952
        904 LLYILFATLEAYCYIKGF 921
Qу
           1111 1::1111:111
Db
        953 LLYIFFSSLEAYCHIKGF 970
RESULT 2
S43730
Na+/Ca2+-exchanging protein - rat
C; Species: Rattus norvegicus (Norway rat)
C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text change 18-Aug-2000
C; Accession: S43730
R; Furman, I.; Cook, O.; Kasir, J.; Rahamimoff, H.
FEBS Lett. 319, 105-109, 1993
A; Title: Cloning of two isoforms of the rat brain Na(+)-Ca(2+) exchanger gene
and their functional expression in HeLa cells.
A; Reference number: S32435; MUID: 93202244; PMID: 8454039
A; Accession: S43730
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-935 <FUR>
A;Cross-references: EMBL:X68812; NID:g288229; PIDN:CAA48707.1; PID:g288230
C; Superfamily: human Na+/Ca2+-exchanging protein
                     71.7%; Score 3441; DB 2; Length 935;
 Query Match
 Best Local Similarity
                     71.1%; Pred. No. 2.7e-223;
 Matches 673; Conservative 109; Mismatches 123; Indels
                                                               11;
                                                     42;
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Qy '
                : : | | | | |
                                        11 11:
          2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN----ETTECTGSYYCK 53
Db
         56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
Qу
           54 KGVILPIWEPODPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSOEKEITIK 113
Db
        116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 175
Qу
           114 KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA 173
Db
Qy
        176 FNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL 235
           174 FNMFIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL 233
Db
Qу
        236 LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMM 292
           Db
        234 LTFFFFPICVVFAWVADRRLLFYKYVYKRYRAGKQRGMIIEHEGDRPASKTEIEMDGKVV 293
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Qу	293	NSHFLDGNLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS 345
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Qy	346	HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412
Qу	405	YQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
Db	413	YQCLENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472
Qу	465	SVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
Db	473	RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDGILDSNHVSAIACLGSPNTATITI 528
Qy	524	LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
Db	529	FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588
Qу	584	YGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERGISDVTDR 634
Db	589	CGELEFQNDEIVKTISVKVIDDEEYEKNKTFFIEIGEPRLVEMSEKKGGFTLTEEYDDKQ 648
Qу	635	KLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRD 694
Db	649	PLTSKEEEERRIAEMGRPILGEHTKLEVIIEESYEFKSTVDKLIKKTNLALVVGTNSWRE 708
Qy	695	QFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAV 754
Db	709	QFIEAITVSAGEDDDDDECGEEKLPSCFDYVMHFLTVFWKVLFAFVPPTEYWNGWACFIV 768
Qу	755	SILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADAS 814
Db	769	SILMIGLLTAFIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTFASKVAATQDQYADAS 828
Qy	815	IGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLL 874
Db	829	IGNVTGSNAVNVFLGIGVAWSIAAIYHAANGEQFKVSPGTLAFSVTLFTIFAFINVGVLL 888
Qy	875	YRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
Db	889	YRRRPEIGGELGGPRTAKLLTSSLFVLLWLLYIFFSSLEAYCHIKGF 935

RESULT 3 S32815

Na+/Ca2+-exchanging protein - human

N; Alternate names: Na+/Ca2+ antiporter; Na+/Ca2+ exchanger

C; Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000

C; Accession: S32815; A56767

R; Komuro, I.; Wenninger, K.E.; Philipson, K.D.; Izumo, S.

Proc. Natl. Acad. Sci. U.S.A. 89, 4769-4773, 1992

A; Title: Molecular cloning and chsracterization of the human cardiac

Na(+)/Ca(2+) exchanger cDNA.

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A; Reference number: S32815; MUID: 92262521; PMID: 1374913
A; Accession: S32815
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-973 <IZU>
A; Cross-references: EMBL: M91368; NID: q180672; PIDN: AAA35702.1; PID: q180673
R; Kofuji, P.; Hadley, R.W.; Kieval, R.S.; Lederer, W.J.; Schulze, D.H.
Am. J. Physiol. 263, C1241-C1249, 1992
A; Title: Expression of the Na-Ca exchanger in diverse tissues: a study using the
cloned human cardiac Na-Ca exchanger.
A; Reference number: A56767; MUID: 93118744; PMID: 1476165
A; Accession: A56767
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 4-253, 'K', 255-627, 'K', 629-692, 'K', 694-973 < KOF>
A; Note: sequence extracted from NCBI backbone (NCBIN:121726, NCBIP:121727)
C; Superfamily: human Na+/Ca2+-exchanging protein
C; Keywords: cardiac muscle; heart; phosphoprotein; transmembrane protein
                      71.7%; Score 3439.5; DB 2; Length 973;
 Query Match
 Best Local Similarity
                      68.9%; Pred. No. 3.6e-223;
 Matches 674; Conservative 111; Mismatches 128; Indels
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                                                                 10;
Qy
          1 MAWLRLQPLTSAFLHFGLVTFVLF--LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
            | | | | | | : : : | |
                                          1:
                                               11:
          4 MRRLSLSPTFSMGFHLLVTVSLLFSHVDHVIAETEMEGEGNETGE----CTGSYYCKKGV 59
Db
Qу
         59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPN 118
            60 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN 119
Db
        119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM 178
Qу
            Db
        120 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 179
        179 FIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL 238
Qу
            180 FIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF 239
Db
Qу
        239 FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH 295
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Db
        240 FFFPICVVFAWVADRRLLFYKYVYKRYRAGKQRGMIIEHEGDRPSSKTEIEMDGKVVNSH 299
Qy
        296 ---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 348
              300 VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLSQQQ 358
Db
Qу
        349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYOC 407
            359 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVTENDPVSKIFFEQGTYQC 418
Db
        408 LENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
Οv
            419 LENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGDTQKEIRVG 478
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Qу

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Db
        479 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD 535
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Qу
                     Db
        536 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 595
        588 EFKNDETVKTIRVKIVDEEEYEROENFFIALGEPKWMERG------ 627
Qу
           Db
        596 EFQNDEIVKTISVKVIDDEEYEKNKTFFLEIGEPRLVEMSEKKALLLNELGGFTITGKYL 655
        628 -----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGEHPKLEVI 663
Qy
                              Dh
        656 FGQPVFRKVHAREHPILSTVITIADEYDDKQPLTSKEEEERRIAEMGRPILGEHTKLEVI 715
        664 IEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFD 723
Qy
           716 IEESYEFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKLPSCFD 775
Db
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Db
        784 TAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWAL 843
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           836 TAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAA 895
Db
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            Db
        896 NGEQFKVSPGTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSCLFVLLW 955
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Qу
           Db
        956 LLYIFFSSLEAYCHIKGF 973
RESULT 4
B53335
Na+/Ca2+-exchanging protein NCX1, splice form NACA6 - rabbit
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 06-Oct-1994 #sequence revision 18-Nov-1994 #text change 18-Aug-2000
C; Accession: B53335
R; Kofuji, P.; Lederer, W.J.; Schulze, D.H.
J. Biol. Chem. 269, 5145-5149, 1994
A; Title: Mutually exclusive and cassette exons underlie alternatively spliced
isoforms of the Na/Ca exchanger.
A; Reference number: A53335; MUID: 94148976; PMID: 8106495
A:Accession: B53335
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-941 <KOF>
A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIP:144050)
C; Superfamily: human Na+/Ca2+-exchanging protein
                     71.7%; Score 3437.5; DB 2; Length 941;
 Query Match
 Best Local Similarity
                     71.0%; Pred. No. 4.7e-223;
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Matches 669; Conservative 111; Mismatches 125; Indels

37; Gaps

11;

Qу	8	PLTSAFLHFGLVTFVLF-LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPE	66
Db	9	: : :: : : : : : :	64
Qу	67	NPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTI:	126
Db	65	DPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKK-NGETTKTTV	123
Qу	127	RVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICV :	186
Db	124	RIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIIALCV	183
Qу	187	YVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVL	246
Db	184	YVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVISPGIVEVWEGLLTFFFFPICVV	243
Qу	247	LAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	244	FAWVADRRLLFYKYVYKRYRAGKQRGMIIEHEGDRPSSKTEIEMDGKVVNSHVDNFLDGA	303
Qу	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRI	356
Db	304	LV-LDVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQKSRAFYRI	362
Qу	357	QATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLENCGAVL	415
Db	363	QATRLMTGAGNILKRHAADQARKAVSMHEVNTEMAENDPVSKIFFEQGTYQCLENCGTVA	422
QУ	416	LTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFE	475
Db	423	LTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVGIIDDDIFE	482
Qу	476	EDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFE	535
Db	483	EDENFLVHLSNVKVSSETSEDGILEANHISTLACLGSPCTATVTIFDDDHAGIFTFE	539
Qу	536	CDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	540	ESVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGELEFQNDEIV	599
Qу	596	KTIRVKIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTME	639
Db	600	KTISVKVIDDEEYEKNKTFFLEIGEPRLVEMSEKKALLLNELGGFTITEEYDDKQPLTSK	659
QУ	640	EEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEA	699
Db	660	EEEERRIAEMGRPILGEHTKLEVIIEESYEFKSTVDKLIKKTNLALVVGTNSWREQFIEA	719
QУ	700	ITVSAAGDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILII	759
Db	720	ITVSAGEDDDDDECGEEKLPSCFDYVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMI	779
Qу	760	GMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVT	819
Db	780	GLTAFIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTFASKVAATQDQYADASIGNVT	839

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820 GSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRP 879
Qу
          840 GSNAVNVFLGIGVAWSIAAIYHAANGEHFKVSPGTLAFSVTLFTIFAFINVGVLLYRRRP 899
Db
        880 HLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
Qу
             900 EIGGELGGPRTAKLLTSCLFVLLWLLYIFFSSLEAYCHIKGF 941
Db
RESULT 5
S32435
Na+/Ca2+-exchanging protein RBE-2 - rat
N; Alternate names: Na+/Ca2+ antiporter; sodium-calcium exchanger RBE-2
C; Species: Rattus norvegicus (Norway rat)
C; Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 18-Aug-2000
C; Accession: S32435
R; Furman, I.; Cook, O.; Kasir, J.; Rahamimoff, H.
FEBS Lett. 319, 105-109, 1993
A; Title: Cloning of two isoforms of the rat brain Na(+)-Ca(2+) exchanger gene
and their functional expression in HeLa cells.
A; Reference number: S32435; MUID: 93202244; PMID: 8454039
A; Accession: S32435
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-958 <FUR>
A;Cross-references: EMBL:X68813; NID:q288231; PIDN:CAA48708.1; PID:q288232
C; Superfamily: human Na+/Ca2+-exchanging protein
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                      71.6%; Score 3434.5; DB 2; Length 958;
 Best Local Similarity
                      69.6%; Pred. No. 7.6e-223;
 Matches 675; Conservative 106; Mismatches 124; Indels
                                                      65; Gaps
                                                                 11;
          4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGONNESCSGSSDCK 55
Qу
                 : : | | | | |
                                         11 11:
          2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53
Db
Qу
         56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
            Db
         54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSOEKEITIK 113
        116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 175
Qy
            114 KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA 173
Db
        176 FNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL 235
Qу
            Db
        174 FNMFIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL 233
        236 LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMM 292
Qу
            Db
        234 LTFFFFPICVVFAWVADRRLLFYKYVYKRYRAGKORGMIIEHEGDRPASKTEIEMDGKVV 293
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Qу
                 Db
        294 NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS 352
        346 HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
QУ
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353 QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412
Db
        405 YQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
Qу
           1111111 1 1 1::1:111:: 1::11::111::111::111::111::111::11
        413 YQCLENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETOKEI 472
Db
        465 SVGIIDDDIFEEDEHFFVRLSNVRIEEEOPEEGMPPAIFNSLPLPR-AVLASPCVATVTT 523
Qy
            473 RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528
Db
Qу
        524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
            Db
        529 FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588
        584 YGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMER---
Qу
            11111:111 1111 11::1:1111: : 111 :111: :1
        589 CGELEFQNDEIVKTISVKVIDDEEYEKNKTFFIEIGEPRLVEMSEKKGGFTLTGQPVFRK 648
Db
       627 -----GISDVTDRK--LTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFK 671
Qу
                      11: 1 1 11:111:1111:1:1111 11:11111
Db
        649 VHARDHPIPSTVISISEEYDDKQPLTSKEEEERRIAEMGRPILGEHTKLEVIIEESYEFK 708
       672 TTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTV 731
Qy
           709 STVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKLPSCFDYVMHFLTV 768
Db
       732 FWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAF 791
Qу
           769 FWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSVTAVVFVAL 828
Db
       792 GTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVS 851
Qу
           829 GTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAANGEOFKVS 888
Db
       852 AGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFAT 911
Qу
            889 PGTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSSLFVLLWLLYIFFSS 948
Db
       912 LEAYCYIKGF 921
Qу
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Db
       949 LEAYCHIKGF 958
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RESULT 6

Na+/Ca2+-exchanging protein - guinea pig
C; Species: Cavia porcellus (quinea pig)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text change 18-Aug-2000

C; Accession: I48097

R; Tsuruya, Y.; Bersohn, M.M.; Li, Z.; Nicoll, D.A.; Philipson, K.D.

Biochim. Biophys. Acta 1196, 97-99, 1994

A; Title: Molecular cloning and functional expression of the guinea pig cardiac Na(+)-Ca2+ exchanger.

A; Reference number: I48097; MUID: 95078257; PMID: 7986817

A; Accession: I48097

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA A; Residues: 1-970 < RES>

A; Cross-references: EMBL: U04955; NID: g927230; PIDN: AAA73904.1; PID: g507350

C; Superfamily: human Na+/Ca2+-exchanging protein

Query Match 71.6%; Score 3432.5; DB 2; Length 970; Best Local Similarity 68.7%; Pred. No. 1.1e-222; Matches 672; Conservative 112; Mismatches 129; Indels 65; Gaps 11; 1 MAWLRLQPLTSAFLH-FGLVTFVL-FLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58 Qу ::| :: :: : || :: | Db 1 MLRLSLSPTYSLGFHLLAMMTLLISHVDHITAET----EMVEEGNETGECTGSYYCKKGV 56 59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN 118 Qу 57 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN 116 Db 119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM 178 Qy 117 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 176 Db 179 FIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL 238 Qу 177 FIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF 236 Db 239 FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH 295 Qy 237 FFFPICVVFAWVADRRLLFYKYVYKRYRAGKORGMIIEHEGDRPSSKTEIEMDGKVVNSH 296 Db 296 ---FLDGNLVPLEGKEVD----ESRREMIRILKDLKOKHPEKDLDOLVEMANYYALSHOO 348 Qy 297 VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355 Db Qy 349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYOC 407 Db 356 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTYQC 415 408 LENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETOKEFSVG 467 Qy 11111 | 11::1:111:: 1::111:111:111:1111:1111 | 1111111 | 1111111 | 11 416 LENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475 Db 468 IIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527 Qу 476 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHIS---TLACLGSPSTATVTIFDDD 532 Db 528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587 QУ 533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592 Db 588 EFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG------ 627 Qу 1|:||| |||| |||::|:||||:::||:::|| 593 EFQNDEIVKTISVKVIDDEEYEKNKTFFLEIGEPRLVEMSEKKALLLNELGGFTITGKHL 652 Db Qу -----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGEHPKLEVI 663 1:| | | | | | :||| :||||:|:|:||| Db 653 YGQPVLRKVHARDHPIPSTVITIADEYDDKQPLTSKEEEERRIAELGRPILGEHTKLEVI 712

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664 IEESYEFKTTVDKLIKKTNLALVVGTHSWRDOFMEAITVSAAGDEDEDESGEERLPSCFD 723
Qу
             Db
         713 IEESYEFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKLPSCFD 772
         724 YVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSV 783
Qy
             773 YVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSV 832
Db
         784 TAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWAL 843
Qy
             833 TAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAA 892
Db
         844 QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLW 903
Qу
             Db
         893 NGEQFKVSPGTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSCLFVLLW 952
         904 LLYILFATLEAYCYIKGF 921
Qу
             1111 1::1111::111
Db
         953 LLYIFFSSLEAYCHIKGF 970
RESULT 7
A53789
Na+/Ca2+-exchanging protein precursor, splice form NACA7 - rat
C; Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1995 #sequence revision 01-Dec-1995 #text change 18-Aug-2000
C; Accession: A53789; JX0288
R; Lee, S.L.; Yu, A.S.L.; Lytton, J.
J. Biol. Chem. 269, 14849-14852, 1994
A; Title: Tissue-specific expression of Na(+)-Ca(2+) exchanger isoforms.
A; Reference number: A53789; MUID: 94253030; PMID: 8195112
A; Accession: A53789
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-957 <LEE>
A; Cross-references: GB: U04933; NID: q451571; PIDN: AAB39952.1; PID: q451572
R; Nakasaki, Y.; Iwamoto, T.; Hanada, H.; Imagawa, T.; Shiqekawa, M.
J. Biochem. 114, 528-534, 1993
A; Title: Cloning of the rat aortic smooth muscle Na+/Ca2+ exchanger and tissue-
specific expression of isoforms.
A; Reference number: JX0288; MUID: 94103175; PMID: 8276763
A; Accession: JX0288
A; Molecule type: mRNA
A; Residues: 1-957 < NAK>
A; Experimental source: aortic smooth muscle
C; Superfamily: human Na+/Ca2+-exchanging protein
C; Keywords: ion transport; membrane protein
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-957/Product: Na+/Ca2+ exchanger #status predicted <MAT>
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 Query Match
 Best Local Similarity
                       69.6%; Pred. No. 2.8e-222;
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                                                          64; Gaps
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Qу
           4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK 55
                   : : | | | | | |
                                            11 11:
                                                            1:11 11
Db
          2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53
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Qу	56	EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK : :: ::	115
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK	113
Qу	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA	175
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qу	176	FNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL	235
Db	174	FNMFIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL	233
QУ	236	LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMM	292
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QУ	293	NSHFLDGNLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS	345
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QУ	346	HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT	412
QУ	405	YQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
Db	413	YQCLENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
QУ	465	SVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
Db	473	RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDGILDSNHVSAIACLGSPNTATITI	528
QУ	524	LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT	583
Db	529	FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT	588
Qу	584	YGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG	627
Db	589	CGELEFQNDEIVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKGGFTLTGQPVFRKV	648
Qу	628	ISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKT	672
Db	649	HARDHPIPSTVISISEEYDDKQPLTSKEEEERRIAEMGRPILGEHTKLEVIIEESYEFKS	708
QУ	673	TVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVF	732
Db	709	TVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKLPSCFDYVMHFLTVF	768
Qу	733	WKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFG	792
Db	769	WKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSVTAVVFVALG	828
QУ	793	TSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSA	852
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Qу
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         949 EAYCHIKGF 957
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S27114
Na+/Ca2+-exchanging protein precursor, cardiac - bovine
N; Alternate names: Na+/Ca2+ antiporter
C; Species: Bos primigenius taurus (cattle)
C;Date: 22-Nov-1993 #sequence revision 23-Mar-1995 #text change 18-Aug-2000
C; Accession: S27114; S18388
R; Aceto, J.F.; Condrescu, M.; Kroupis, C.; Nelson, H.; Nelson, N.; Nicoll, D.;
Philipson, K.D.; Reeves, J.P.
Arch. Biochem. Biophys. 298, 553-560, 1992
A; Title: Cloning and expression of the bovine cardiac sodium-calcium exchanger.
A; Reference number: S27114; MUID: 93037494; PMID: 1416984
A; Accession: S27114
A; Molecule type: mRNA
A; Residues: 1-970 <ACE>
A; Cross-references: GB: L06438; NID: q163033; PIDN: AAA30509.1; PID: q163034
R; Durkin, J.T.; Ahrens, D.C.; Pan, Y.C.E.; Reeves, J.P.
Arch. Biochem. Biophys. 290, 369-375, 1991
A; Title: Purification and amino-terminal sequence of the bovine cardiac sodium-
calcium exchanger: evidence for the presence of a signal sequence.
A; Reference number: S18388; MUID: 92027750; PMID: 1929404
A:Accession: $18388
A; Molecule type: protein
A; Residues: 33-40, 'X', 42-44 < DUR>
A; Experimental source: heart
C; Superfamily: human Na+/Ca2+-exchanging protein
C; Keywords: cardiac muscle; heart; ion transport; membrane protein
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-970/Product: Na+/Ca2+ exchange protein, cardiac #status predicted <MAT>
                        71.4%; Score 3425.5; DB 2; Length 970;
 Query Match
                        68.7%; Pred. No. 3.1e-222;
 Best Local Similarity
 Matches 672; Conservative 110; Mismatches 131; Indels
                                                            65; Gaps
                                                                       10;
           1 MAWLRLQPLTSAFLHFGLVTFVLF--LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
Qу
                 : :|| :: : ||
                                               |:
                                                    11:
Db
           1 MLQFSLSPTLSMGFHVIAMVALLFSHVDHISAETEMEGEGNETGE----CTGSYYCKKGV 56
          59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN 118
Qv
             57 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN 116
Db
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Qу
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Db	177	FIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTF 2	36
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Db	237	FFFPICVVFAWVADRRLLFYKYVYKRYRAGKQRGMIIEHEGDRPSSKTEIEMDGKVVNSH 2	96
Qy	296	FLDGNLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 3	48
Db	297	VDSFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 3	55
Qу	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 4	07
Db	356	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTYQC 4	15
Qу	408	LENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 4	67
Db	416	LENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 4	75
Qу	468	IIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 52	27
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Db	533	HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 5	92
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Db		NGEQFKVSPGTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSCLFVLLW 9	52
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Db	953	LLYIFFSSLEAYCHIKGF 970	

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Na+/Ca2+-exchanging protein - rat
N; Alternate names: Na+/Ca2+ antiporter; Na+/Ca2+ exchanger
C; Species: Rattus norvegicus (Norway rat)
C; Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 18-Aug-2000
C; Accession: S28833; S25552
R; Low, W.; Kasir, J.; Rahamimoff, H.
FEBS Lett. 316, 63-67, 1993
A; Title: Cloning of the rat heart Na(+)-Ca(2+) exchanger and its functional
expression in HeLa cells.
A; Reference number: S28833; MUID: 93138118; PMID: 8422940
A; Accession: S28833
A; Molecule type: mRNA
A; Residues: 1-971 <LOW>
A; Cross-references: EMBL: X68191; NID: q57208; PIDN: CAA48273.1; PID: q57209
R; Low, W.; Kasir, J.; Boulter, J.; Heinemann, S.; Rahamimoff, H.
submitted to the EMBL Data Library, August 1992
A; Reference number: S25552
A; Accession: S25552
A; Molecule type: mRNA
A; Residues: 1-194, 'F', 196-971 <LO2>
A; Cross-references: EMBL: X68191
C; Superfamily: human Na+/Ca2+-exchanging protein
C; Keywords: ion transport; membrane protein; phosphoprotein
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 Best Local Similarity 68.6%; Pred. No. 5.4e-222;
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Qy
                 : : | ||| |
                                          11 11:
                                                          1:11
Db
          2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53
         56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
Qу
            Db
         54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK 113
        116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 175
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        114 KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA 173
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        174 FNMFIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL 233
        236 LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMM 292
Qу
            234 LTFFFFPICVVFAWVAARRLLFYKYVYKRYRAGKORGMIIEHEGDRPASKTEIEMDGKVV 293
Db
        293 NSH---FLDGNLVPLEGKEVD----ESRREMIRILKDLKOKHPEKDLDQLVEMANYYALS 345
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Qу
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        353 QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDAVSKVFFEQGT 412
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Qу
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Db
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Qу
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A54139

Na+/Ca2+-exchanging protein NCX2 - rat

C; Species: Rattus norvegicus (Norway rat)

C; Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text change 18-Aug-2000

C; Accession: A54139

R; Li, Z.; Matsuoka, S.; Hryshko, L.V.; Nicoll, D.A.; Bersohn, M.M.; Burke, E.P.; Lifton, R.P.; Philipson, K.D.

J. Biol. Chem. 269, 17434-17439, 1994

A; Title: Cloning of the NCX2 isoform of the plasma membrane Na(+)-Ca(2+)

exchanger.

A; Reference number: A54139; MUID: 94292496; PMID: 8021246

A; Accession: A54139 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-921 <LIA>

A;Cross-references: GB:U08141; NID:g511680; PIDN:AAA19920.1; PID:g511681

C; Superfamily: human Na+/Ca2+-exchanging protein

.C; Keywords: transmembrane protein

Query Match 70.0%; Score 3357; DB 2; Length 921; Best Local Similarity 69.6%; Pred. No. 1.2e-217; 635; Conservative 130; Mismatches 114; Indels 34; 9; Gaps 31 EAGGSGDVPSTGONNE----SCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALI 85 Qy 11 : :1 1: 21 EATPTPSLPPPPANDSDASPGGCQGSYRCOPGVLLPVWEPDDPSLGDKAARAVVYFVAMV 80 Db Qу 86 YMFLGVSIIADRFMASIEVITSOEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSA 145 81 YMFLGLSIIADRFMASIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSA 140 Db 146 PEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFI 205 Qy 141 PEILLSVIEVCGHNFQAGELGPGTIVGSAAFNMFVVIAVCVYVIPAGESRKIKHLRVFFV 200 Db 206 TAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKY 265 Qy Db 201 TASWSIFAYVWLYLILAVFSPGVVQVWEALLTLVFFPVCVVFAWMADKRLLFYKYVYKRY 260 266 RTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGNL----VPLEGKEVDESRREMIRIL 320 Qy 1 | :|:| ||||:|:|| 261 RTDPRSGIIIGAEGDPPKSIELDGTFVGTE-VPGELGALGTGPAEARELDASRREVIOIL 319 Db 321 KDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKA 380 Qу 320 KDLKQKHPDKDLEQLVGIAKYYALLHQQKSRAFYRIQATRLMTGAGNVLRRHAADAARRP 379 Dh 381 SSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSA 440 Qу 1: :1 Db 380 GA-NDGAPDDEDDGASRIFFEPSLYHCLENCGSVLLSVACOGGEGNSTFYVDYRTEDGSA 438 441 NAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEQ----PEE 496 Qу 11:11::11: 11:1: 1:1: : 1 439 KAGSDYEYSEGTLVFKPGETOKELRIGIIDDDIFEEDEHFFVRLLNLRVGDAOGMFEPDG 498 Db 497 GMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTS 556 Qу 1: 1:1:1111111111111:1: :|||| :| ::|:|:|:| 499 G-----GRPKGRLVAPLLATVTILDDDHAGIFSFODRLLHVSECMGTVDVRVVRSS 549 Db 557 GARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFI 616 Qy 550 GARGTVRLPYRTVDGTARGGGVHYEDACGELEFGDDETMKTLQVKIVDDEEYEKKDNFFI 609 Db 617 ALGEPKWMERGISDVT-----DRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEF 670 Qy 11:1:1::1111 : 11111 11111:11111111111: :1111111:1 610 ELGQPQWLKRGISALLLNQGDGDRKLTAEEEEAQRIAEMGKPVLGENCRLEVIIEESYDF 669 Db 671 KTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG--EERLPSCFDYVMHF 728 Qy Dh 670 KNTVDKLIKKTNLALVIGTHSWREQFLEAVTVS-AGDEEEDEDGSREERLPSCFDYVMHF 728 729 LTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVF 788 Qу

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C; Species: Caenorhabditis elegans
C; Date: 10-May-2001 #sequence revision 10-May-2001 #text change 24-May-2001
C; Accession: B89047
R; anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A; Title: Genome sequence of the nematode C. elegans: a platform for
investigating biology.
A; Reference number: A75000; MUID: 99069613; PMID: 9851916
A; Note: see websites genome.wustl.edu/gsc/C elegans/ and
www sanger.ac.uk/Projects/C elegans/ for a list of authors
A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103,
1999; and Science 285, 1493, 1999
A; Accession: B89047
A; Status: preliminary
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A; Residues: 1-890 <STO>
A; Cross-references: GB:chr V; PIDN: AAB09172.1; PID:g1572830; GSPDB:GN00023;
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C; Genetics:
A; Gene: C10G8.5
A; Map position: 5
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Db 229 NPHITPTELQKQAEYEMISRGPKSRAFYRVQATRRLIGGGDIVKKRIDKEHNKALDALVQ 288
Qy 386 VHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGAD 445
Db 289 AQEKQSRDNTCKIFLDPAHYTVLESVGSFDVVVGRDGGPDGLTVMVDYFTEDGSANAGSD 348
Qy 446 YEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIF 503
Db 349 YIPVKGTLTFYPEDKHQKVTIEVVDDDVFEEDEHFYLRLCNLRVRTKDGIIIDPTRI 405
Qy 504 NSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVI 563
Db 406 GGLPVAQLEMPNTATIMILDDDHAGVFGFEHDHFQVVENCGHLSLQMKRHSGARGKVI 463
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hypothetical protein ZC168.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans

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C; Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 29-Oct-1999
C; Accession: T24110; T27507
R; Berks, M.
submitted to the EMBL Data Library, March 1996
A; Reference number: Z19841
A; Accession: T24110
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-807 <WIL>
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A; Experimental source: clone R102
R; Berks, M.
submitted to the EMBL Data Library, March 1996
A; Reference number: Z20378
A; Accession: T27507
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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A;Cross-references: EMBL: Z70312; PIDN: CAA94387.1; GSPDB: GN00022; CESP: ZC168.1
A; Experimental source: clone ZC168
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A; Gene: CESP: ZC168.1
A; Map position: 4
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Qу
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         156 CGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYI 215
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         269 -KHRGIIIETEGDHPKGIEMDGKMMNSHFL----DGNLVPLEGKEVDESRREMIRILKDL 323
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         324 KQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSM 383
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I52640
cardiac sodium/calcium exchanger, cerebellar granule neurons - rat (fragment)
C; Species: Rattus sp. (rat)
C;Date: 27-Feb-1997 #sequence revision 27-Feb-1997 #text change 18-Aug-2000
C; Accession: I52640
R; Marlier, L.N.; Zheng, T.; Tang, J.; Grayson, D.R.
Brain Res. Mol. Brain Res. 20, 21-39, 1993
A; Title: Regional distribution in the rat central nervous system of a mRNA
encoding a portion of the cardiac sodium/calcium exchanger isolated from
cerebellar granule neurons.
A; Reference number: I52640; MUID: 94077033; PMID: 8255180
A; Accession: I52640
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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A; Cross-references: GB:S67769; NID:g459304
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C; Keywords: cardiac muscle; heart
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S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.
submitted to the EMBL Data Library, October 1998
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A; Experimental source: cultivar Columbia
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G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser,
C.M.; Venter, J.C.
Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis
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R; Yu, A.S.; Hebert, S.C.; Lee, S.L.; Brenner, B.M.; Lytton, J.
Am. J. Physiol. 263, F680-F685, 1992
A; Title: Identification and localization of renal Na(+)-Ca2+ exchanger by
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Job time : 24.9182 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2004, 16:12:03; Search time 50.8014 Seconds

(without alignments)

5118.180 Million cell updates/sec

Title: US-10-054-680-2

Perfect score: 4797

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Searched: 1163542 seqs, 282313646 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4	4686	97.7	927	9	US-09-804-474A-4	Sequence 4, Appli
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ALIGNMENTS

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 ; Patent No. US20020119518A1
- ; GENERAL INFORMATION:
- ; APPLICANT: KODET, Stefan et al

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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
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  TITLE OF INVENTION: AND USES THEREOF
  FILE REFERENCE: CL000891
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  CURRENT FILING DATE: 2001-03-13
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  APPLICANT: Hilbun, Erin
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  CURRENT FILING DATE: 2002-01-22
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Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120	
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180	
Db	121		
Qу	181	IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240	
Db	181	IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240	
<u> Qy</u>	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300	
Db	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300	
Qy	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360	
Db	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360	
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420	
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420	
Qy	421	KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480	
Db	421	KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480	
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540	
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540	
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600	
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600	
Qy	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL 660	
Db	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL 660	
Qy	661	EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720	
Db	661	EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720	
Qу	721	CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780	
Db	721	CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780	
Qу	781	DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840	
Db	781	DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840	
Qy	841	WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900	
Db	841	WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900	

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901 SLWLLYILFATLEAYCYIKGF 921
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Db
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US-10-275-116-2
; Sequence 2, Application US/10275116
: Publication No. US20030096312A1
 GENERAL INFORMATION:
  APPLICANT: Merck Patent GmbH
  TITLE OF INVENTION: No. US20030096312A1el natrium-calium exchanger protein
  FILE REFERENCE: HNCX3CWWS
  CURRENT APPLICATION NUMBER: US/10/275,116
  CURRENT FILING DATE: 2002-11-01
  NUMBER OF SEQ ID NOS: 2
  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
   LENGTH: 927
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-275-116-2
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                     99.7%;
                           Score 4784; DB 14;
                                           Length 927;
 Best Local Similarity
                     99.4%; Pred. No. 0;
 Matches 921; Conservative
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                          0; Mismatches
                                            Indels
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Qу
           Db
         61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPNGE 120
        121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
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Db
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Qу
           Db
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           661 GEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 720
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        715 EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFG 774
Qу
           Db
        721 EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFG 780
        775 CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 834
Qy
           Db
        781 CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALODVYADASIGNVTGSNAVNVFLGIGLAW 840
        835 SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLA 894
Qу
           Db
        841 SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLA 900
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RESULT 4
US-09-804-474A-4
; Sequence 4, Application US/09804474A
; Patent No. US20020119518A1
; GENERAL INFORMATION:
  APPLICANT: KODET, Stefan et al
  TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
PROTEINS,
  TITLE OF INVENTION: AND USES THEREOF
  FILE REFERENCE: CL000891
  CURRENT APPLICATION NUMBER: US/09/804,474A
  CURRENT FILING DATE: 2001-03-13
  NUMBER OF SEQ ID NOS: 4
  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
   LENGTH: 927
   TYPE: PRT
   ORGANISM: Rat
US-09-804-474A-4
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Query Match 97.7%; Score 4686; DB 9; Length 927;

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1	Qу	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
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	Qу	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR	360
	Db	301	LIPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR	360
	Qу	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
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	Db	421	KGGDISKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF	480
	Qу	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
	Db	481	FVRLSNVRVEEEQLEEGMTPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
	Qу	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV	600

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601 KIVDEEEYERQENFFIALGEPKWMERGISALLLSPEVTDRKLTMEEEEAKRIAEMGKPVL 660

655 GEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 714

715 EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFG 774

721 EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFVVSILIIGMLTAIIGDLASHFG 780

775 CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 834

Db

Qу

Db

Qу

Db

Qу

Db

Qу

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US-10-114-153-4
; Sequence 4, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
  APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
  APPLICANT: Guo, Xiaojia
  APPLICANT: Gerlach, Valerie
APPLICANT: Casman, Stacie
;
  APPLICANT: Boldog, Ferenc
  APPLICANT: Li, Li
  APPLICANT: Zerhusen, Bryan
  APPLICANT: Tchernev, Velizar
  APPLICANT: Gangolli, Esha
  APPLICANT: Vernet, Corine
  APPLICANT: Spytek, Kimberly APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
  APPLICANT: Miller, Charles
  APPLICANT: Taupier, Raymond J. Jr.
  APPLICANT: Heyes, Melvyn
  APPLICANT: Ju, Jingfang
  APPLICANT: Peyman, John
  APPLICANT: Catterton, Elina APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
  APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
  TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
  TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
   FILE REFERENCE: 21402-322A
  CURRENT APPLICATION NUMBER: US/10/114,153
  CURRENT FILING DATE: 2002-08-06
   PRIOR APPLICATION NUMBER: 60/281086
   PRIOR FILING DATE: 2001-04-03
  PRIOR APPLICATION NUMBER: 60/281906
   PRIOR FILING DATE: 2001-04-05
   PRIOR APPLICATION NUMBER: 60/282020
  PRIOR FILING DATE: 2001-04-06
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PRIOR APPLICATION NUMBER: 60/282930

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PRIOR FILING DATE: 2001-04-10
  PRIOR APPLICATION NUMBER: 60/283512
  PRIOR FILING DATE: 2001-04-12
  PRIOR APPLICATION NUMBER: 60/283444
  PRIOR FILING DATE: 2001-04-12
  PRIOR APPLICATION NUMBER: 60/283657
  PRIOR FILING DATE: 2001-04-13
  PRIOR APPLICATION NUMBER: 60/283710
  PRIOR FILING DATE: 2001-04-13
  PRIOR APPLICATION NUMBER: 60/283678
  PRIOR FILING DATE: 2001-04-13
  PRIOR APPLICATION NUMBER: 60/284234
  PRIOR FILING DATE: 2001-04-17
  Prior Application data removed - See File Wrapper or PALM.
  NUMBER OF SEQ ID NOS: 251
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   LENGTH: 925
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-114-153-4
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                            Score 4671; DB 14; Length 925;
                     96.9%; Pred. No. 0;
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Db
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Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540)
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600	}
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIHI 600)
Qy	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGE 656	;
Db	601	KVIDDEAYEKNKNYFIEMMGPRMVDMSFQKALLLSPDRKLTMEEEEAKRIAEMGKPVLGE 660)
Qу	657	HPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEE 716	;
Db	661	HPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEE 720)
Qу	717	RLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCT 776	;
Db	721	RLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCT 780)
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Db	781	IGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSV 840	ı
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Db	841	AAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATT 900	ŧ
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US-10-114-153-6

- ; Sequence 6, Application US/10114153
- ; Publication No. US20030185815A1
- ; GENERAL INFORMATION:
- ; APPLICANT: Padigaru, Muralidhara
- ; APPLICANT: Shenoy, Suresh
- ; APPLICANT: Kekuda, Ramesh
- ; APPLICANT: Rastelli, Luca
- ; APPLICANT: Mezes, Peter
- ; APPLICANT: Smithson, Glennda
- ; APPLICANT: Guo, Xiaojia
- ; APPLICANT: Gerlach, Valerie
- ; APPLICANT: Casman, Stacie
- ; APPLICANT: Boldog, Ferenc
- ; APPLICANT: Li, Li
- ; APPLICANT: Zerhusen, Bryan
- ; APPLICANT: Tchernev, Velizar
- ; APPLICANT: Gangolli, Esha
- ; APPLICANT: Vernet, Corine
- ; APPLICANT: Spytek, Kimberly
- ; APPLICANT: Malyankar, Uriel
- ; APPLICANT: Patturajan, Meera
- ; APPLICANT: Miller, Charles

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Taupier, Raymond J. Jr.
  APPLICANT:
  APPLICANT:
             Heyes, Melvyn
  APPLICANT:
             Ju, Jingfang
             Peyman, John
  APPLICANT:
             Catterton, Elina
  APPLICANT:
  APPLICANT: MacDougall, John
  APPLICANT: Edinger, Shlomit
  APPLICANT:
             Stone, David
  APPLICANT: Mazur, Ann
  TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
  TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
  FILE REFERENCE: 21402-322A
  CURRENT APPLICATION NUMBER: US/10/114,153
  CURRENT FILING DATE: 2002-08-06
  PRIOR APPLICATION NUMBER: 60/281086
  PRIOR FILING DATE: 2001-04-03
  PRIOR APPLICATION NUMBER: 60/281906
  PRIOR FILING DATE: 2001-04-05
  PRIOR APPLICATION NUMBER: 60/282020
  PRIOR FILING DATE: 2001-04-06
  PRIOR APPLICATION NUMBER: 60/282930
  PRIOR FILING DATE: 2001-04-10
  PRIOR APPLICATION NUMBER: 60/283512
  PRIOR FILING DATE: 2001-04-12
  PRIOR APPLICATION NUMBER: 60/283444
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  PRIOR APPLICATION NUMBER: 60/283678
  PRIOR FILING DATE: 2001-04-13
  PRIOR APPLICATION NUMBER: 60/284234
  PRIOR FILING DATE: 2001-04-17
  Prior Application data removed - See File Wrapper or PALM.
  NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 6
   LENGTH: 895
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-114-153-6
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                       96.8%; Score 4644; DB 14;
                                                  Length 895;
 Best Local Similarity
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            2 SEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL 61
Db
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Qy	210	SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDK	269
Db	182	SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDK	241
Qy	270	HRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRREMIRILKDLKQKHPE	329
Db	242	HRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRREMIRILKDLKQKHPE	301
Qy	330	KDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD	389
Db	302	KDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD	361
Qy	390	EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFT	449
Db	362	EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFT	421
Qy	450	EGTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP	509
Db	422	EGTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP	481
Qy	510	RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTV	569
Db	482	RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTV	541
Qy	570	EGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERGIS	629
Db	542	EGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERGIS	601
QУ	630	DVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGT	689
Db	602	DVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGT	661
QУ	690	HSWRDQFMEAITVSAAGDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGW	749
Db	662	HSWRDQFMEAITVSAAGDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGW	721
QУ	750	ACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDV	809
Db	722	ACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDV	781
Qу	810	YADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVC	869
Db	782	YADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVC	841
Qу	870	ISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921	
Db	842	ISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYTLFATLEAYCYTKGF 893	

US-10-114-153-2

[;] Sequence 2, Application US/10114153 ; Publication No. US20030185815A1

[;] GENERAL INFORMATION:

[;] APPLICANT: Padigaru, Muralidhara

```
APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
 APPLICANT: Rastelli, Luca
  APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
  APPLICANT: Li, Li
;
  APPLICANT: Zerhusen, Bryan
;
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
  APPLICANT: Malyankar, Uriel
  APPLICANT: Patturajan, Meera
APPLICANT: Miller, Charles
;
;
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
  APPLICANT: MacDougall, John
  APPLICANT: Edinger, Shlomit
;
 APPLICANT: Stone, David
;
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
:
  TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
 FILE REFERENCE: 21402-322A
  CURRENT APPLICATION NUMBER: US/10/114,153
  CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
 PRIOR FILING DATE: 2001-04-06
  PRIOR APPLICATION NUMBER: 60/282930
  PRIOR FILING DATE: 2001-04-10
  PRIOR APPLICATION NUMBER: 60/283512
  PRIOR FILING DATE: 2001-04-12
  PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
  PRIOR FILING DATE: 2001-04-13
  PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
  PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
  Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 2
; LENGTH: 928
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; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-114-153-2

Score 4505.5; Query Match 93.9%; DB 14; Length 928; Best Local Similarity 92.8%; Pred. No. 0; 862; Matches Conservative 37; Mismatches 21; Gaps 3; Qу 1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60 Db 1 MAWLRLOPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGONNESCSGSSDCKEGVIL 60 61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120 Qy 61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120 Db 121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180 Qу 121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180 Db 181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240 Qy 181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240 Db Qy 241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300 241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300 Db Qу 301 LVPLEGKEVDESRREMIRILKDLKOKHPEKDLDOLVEMANYYALSHOOKSRAFYRIOATR 360 301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360 Dh 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420 Qу 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420 Db 421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480 Qy 421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480 Db Qу 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540 Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600 Qу 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTLOV 600 Db 601 KIVDEEEYERQENFFIALGEPKWMERGISDVT-----DRKLTMEEEEAKRIAEMGKPVL 654 Qу 1|||| 601 KIVDDEEYEKKDNFFIELGOPOWLKRGISALLLNOGDGDRKLTAEEEEARRIAEMGKPVL 660 Db Qу 655 GEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 714 661 GENCRLEVIIEESYDFKNTVDKLIKKTNLALVIGTHSWREQFLEAITVS-AGDEEEEEDG 719 Db 715 --EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASH 772 Qу

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Db
        720 SREERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFGVSILVIGLLTALIGDLASH 779
        773 FGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGL 832
Qу
           Db
        780 FGCTVGLKDSVNAVVFVALGTSIPDTFASKVAALODOCADASIGNVTGSNAVNVFLGLGV 839
        833 AWSVAAIYWALOGOEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCK 892
Qу
           840 AWSVAAVYWAVQGRPFEVRTGTLAFSVTLFTVFAFVGIAVLLYRRRPHIGGELGGPRGPK 899
Db
Qy
        893 LATTWLFVSLWLLYILFATLEAYCYIKGF 921
           1111 11: 111111111:1111:1:11
Db
        900 LATTALFLGLWLLYILFASLEAYCHIRGF 928
RESULT 8
US-09-901-419-2
; Sequence 2, Application US/09901419
; Patent No. US20020069421A1
; GENERAL INFORMATION:
  APPLICANT: The Curators of the University of Missouri
  TITLE OF INVENTION: LARGE SCALE EXPRESSION AND PURIFICATION OF RECOMBINANT
  TITLE OF INVENTION: PROTEINS
  FILE REFERENCE: UM01531.1
  CURRENT APPLICATION NUMBER: US/09/901,419
  CURRENT FILING DATE: 2001-07-09
  PRIOR APPLICATION NUMBER: 60/218,125
  PRIOR FILING DATE: 2000-01-13
  NUMBER OF SEQ ID NOS: 2
  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
   LENGTH: 970
   TYPE: PRT
   ORGANISM: Bos taurus
US-09-901-419-2
 Query Match
                     71.4%; Score 3425.5; DB 9; Length 970;
 Best Local Similarity 68.7%; Pred. No. 1.7e-305;
 Matches 672; Conservative 110; Mismatches 131; Indels
                                                     65; Gaps
                                                               10;
          1 MAWLRLQPLTSAFLHFGLVTFVLF--LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
Qу
               | | | | : : | | :: : | |
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                                                    1:11 11:11
Db
          1 MLQFSLSPTLSMGFHVIAMVALLFSHVDHISAETEMEGEGNETGE----CTGSYYCKKGV 56
         59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN 118
Qу
           57 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN 116
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        119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM 178
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           117 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 176
Db
        179 FIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL 238
Qу
           Db
        177 FIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTF 236
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Qу	239	FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSH	
Db	237	FFFPICVVFAWVADRRLLFYKYVYKRYRAGKQRGMIIEHEGDRPSSKTEIEMDGKVVNSH	
Qy	296	FLDGNLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ	348
Db	297		355
Qу	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC	407
Db	356	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTYQC	415
Qу	408	LENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
Db	416	LENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG	475
Qy	468	IIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD	527
Db	476	IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVSTLACLGSPSTATVTIFDDD	532
Qу	528	HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL	587
Db	533	HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL	592
Qу	588	EFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG	627
Db	593	EFQNDEIVKTISVKVIDDEEYEKNKTFFLEIGEPRLVEMSEKKALLLNELGGFTITGKYL	652
Qy	628	ISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVI	663
Db	653	YGQPVFRKVHAREHPLPSTIITIADEYDDKQPLTSKEEEERRIAEMGRPILGEHTRLEVI	712
Qy	664	IEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFD	723
Db	713	IEESYEFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKLPSCFD	772
Qy	724	YVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSV	783
Db	773	YVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFACTIALKDSV	832
Qу	784	TAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWAL	843
Db	833	TAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAA	892
Qy	844	QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLW ::	903
Db	893	NGEQFKVSPGTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSCLFVLLW	952
Qy	904	LLYILFATLEAYCYIKGF 921	
Db	953	LLYIFFSSLEAYCHIKGF 970	

US-10-281-866-2

[;] Sequence 2, Application US/10281866 ; Publication No. US20030091570A1

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; GENERAL INFORMATION:
  APPLICANT: Silos-Santiago, Inmaculada
  TITLE OF INVENTION: Methods and compositions for the
  TITLE OF INVENTION: treatment and diagnosis of pain disorders using 46556
  FILE REFERENCE: MPI01-272P1RM
  CURRENT APPLICATION NUMBER: US/10/281,866
  CURRENT FILING DATE: 2002-10-28
  PRIOR APPLICATION NUMBER: 60/335,078
  PRIOR FILING DATE: 2001-10-31
  NUMBER OF SEQ ID NOS: 3
  SOFTWARE: FastSEO for Windows Version 4.0
 SEO ID NO 2
   LENGTH: 921
   TYPE: PRT
   ORGANISM: Homo sapien
US-10-281-866-2
                     70.3%; Score 3373.5; DB 14; Length 921;
 Query Match
 Best Local Similarity
                     71.0%; Pred. No. 9.3e-301;
 Matches 638; Conservative 124; Mismatches 104; Indels
                                                               9;
Qу
         40 STGONNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFM 99
                 Db
         39 STG----GCQGSYRCQPGVLLPVWEPDDPSLGDKAARAVVYFVAMVYMFLGVSIIADRFM 94
Qу
        100 ASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHG 159
           Db
         95 AAIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHN 154
Qу
        160 FIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYM 219
           155 FQAGELGPGTIVGSAAFNMFVVIAVCIYVIPAGESRKIKHLRVFFVTASWSIFAYVWLYL 214
Db
        220 ILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEG 279
Qу
           Db
        215 ILAVFSPGVVQVWEALLTLVFFPVCVVFAWMADKRLLFYKYVYKRYRTDPRSGIIIGAEG 274
        280 DHPKGIEMDGKMMNSHFLDGNL-----VPLEGKEVDESRREMIRILKDLKQKHPEKDLDQ 334
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        275 DPPKSIELDGTFVGAE-APGELGGLGPGPAEARELDASRREVIQILKDLKQKHPDKDLEQ 333
        335 LVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDF 394
Qу
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        334 LVGIANYYALLHOOKSRAFYRIOATRLMTGAGNVLRRHAADASRRAAPAEGAGEDE-DDG 392
        395 ISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVV 454
Qу
            Db
        393 ASRIFFEPSLYHCLENCGSVLLSVTCOGGEGNSTFYVDYRTEDGSAKAGSDYEYSEGTLV 452
        455 LKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEQ----PEEGMPPAIFNSLPLPR 510
Qу
            Db
        453 FKPGETQKELRIGIIDDDIFEEDEHFFVRLLNLRVGDAQGMFEPDGG-----GRPK 503
        511 AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVE 570
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        631 VT-----DRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLA 684
Qу
                  624 LLLNQGDGDRKLTAEEEEARRIAEMGKPVLGENCRLEVIIEESYDFKNTVDKLIKKTNLA 683
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        743 TEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASK 802
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           743 TEYCHGWACFGVSILVIGLLTALIGDLASHFGCTVGLKDSVNAVVFVALGTSIPDTFASK 802
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        803 AAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLF 862
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                 803 VAALQDQCADASIGNVTGSNAVNVFLGLGVAWSVAAVYWAVQGRPFEVRTGTLAFSVTLF 862
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        863 TIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
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           863 TVFAFVGIAVLLYRRRPHIGGELGGPRGPKLATTALFLGLWLLYILFASLEAYCHIRGF 921
Db
RESULT 10
US-10-256-537-2
; Sequence 2, Application US/10256537
; Publication No. US20030162196A1
; GENERAL INFORMATION:
  APPLICANT: Carroll, Joseph M.
  TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
  TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER
  FILE REFERENCE: MPI01-231P1RM
  CURRENT APPLICATION NUMBER: US/10/256,537
  CURRENT FILING DATE: 2002-04-19
  PRIOR APPLICATION NUMBER: 60/325,737
  PRIOR FILING DATE: 2001-09-28
  NUMBER OF SEQ ID NOS: 5
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 2
   LENGTH: 595
   TYPE: PRT
   ORGANISM: Homo sapien
US-10-256-537-2
                     64.5%; Score 3093; DB 14; Length 595;
 Query Match
 Best Local Similarity
                    100.0%; Pred. No. 3e-275;
 Matches 595; Conservative
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121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
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Qу
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        301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
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Db
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        481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
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        481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
        541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
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        541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
RESULT 11
US-10-054-680-4
; Sequence 4, Application US/10054680
; Publication No. US20020132998A1
; GENERAL INFORMATION:
  APPLICANT: Friddle, Carl Johan
  APPLICANT: Hilbun, Erin
  TITLE OF INVENTION: No. US20020132998Alel Human Ion Exchanger Proteins and
Polynucleotides Encoding the
  TITLE OF INVENTION: Same
  FILE REFERENCE: LEX-0301-USA
  CURRENT APPLICATION NUMBER: US/10/054,680
  CURRENT FILING DATE: 2002-01-22
  PRIOR APPLICATION NUMBER: US 60/263,384
  PRIOR FILING DATE: 2001-01-23
  NUMBER OF SEQ ID NOS: 5
  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
   LENGTH: 620
   TYPE: PRT
   ORGANISM: homo sapiens
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US-10-054-680-4

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Query Match
                   64.5%; Score 3093; DB 13; Length 620;
 Best Local Similarity
                   100.0%; Pred. No. 3.2e-275;
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                        0; Mismatches
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                                       Indels
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                                                        0;
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Qy
          1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGONNESCSGSSDCKEGVIL 60
Db
        61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Qу
          61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Db
       121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Qу
          121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Db
       181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qу
          181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVOVWEGLLTLFF 240
Db
       241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qу
          241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Db
Qy
       301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHOOKSRAFYRIOATR 360
          Db
       301 LVPLEGKEVDESRREMIRILKDLKOKHPEKDLDQLVEMANYYALSHOOKSRAFYRIOATR 360
Qу
       361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYOCLENCGAVLLTVVR 420
          Db
       361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
       421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Qу
          Db
       421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETOKEFSVGIIDDDIFEEDEHF 480
       481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qу
          Db
       481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qу
       541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
          Db
       541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
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US-09-864-761-33429

- ; Sequence 33429, Application US/09864761
- ; Patent No. US20020048763A1
- ; GENERAL INFORMATION:
- ; APPLICANT: Penn, Sharron G.
- ; APPLICANT: Rank, David R.
- ; APPLICANT: Hanzel, David K.
- ; APPLICANT: Chen, Wensheng
- ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
- ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

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FILE REFERENCE: Aeomica-X-1
   CURRENT APPLICATION NUMBER: US/09/864,761
   CURRENT FILING DATE: 2001-05-23
   PRIOR APPLICATION NUMBER: US 60/180,312
   PRIOR FILING DATE: 2000-02-04
  PRIOR APPLICATION NUMBER: US 60/207,456
  PRIOR FILING DATE: 2000-05-26
   PRIOR APPLICATION NUMBER: US 09/632,366
   PRIOR FILING DATE: 2000-08-03
   PRIOR APPLICATION NUMBER: GB 24263.6
   PRIOR FILING DATE: 2000-10-04
   PRIOR APPLICATION NUMBER: US 60/236,359
   PRIOR FILING DATE: 2000-09-27
   PRIOR APPLICATION NUMBER: PCT/US01/00666
   PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00667
  PRIOR FILING DATE: 2001-01-30
   PRIOR APPLICATION NUMBER: PCT/US01/00664
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00669
   PRIOR FILING DATE: 2001-01-30
   PRIOR APPLICATION NUMBER: PCT/US01/00665
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00668
   PRIOR FILING DATE: 2001-01-30
   PRIOR APPLICATION NUMBER: PCT/US01/00663
   PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00662
   PRIOR FILING DATE: 2001-01-30
   PRIOR APPLICATION NUMBER: PCT/US01/00661
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: PCT/US01/00670
  PRIOR FILING DATE: 2001-01-30
  PRIOR APPLICATION NUMBER: US 60/234,687
  PRIOR FILING DATE: 2000-09-21
  PRIOR APPLICATION NUMBER: US 09/608,408
  PRIOR FILING DATE: 2000-06-30
  PRIOR APPLICATION NUMBER: US 09/774,203
  PRIOR FILING DATE: 2001-01-29
  NUMBER OF SEQ ID NOS: 49117
   SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33429
   LENGTH: 609
;
   TYPE: PRT
   ORGANISM: Homo sapiens
   FEATURE:
   OTHER INFORMATION: MAP TO AC007281.3
   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.68
   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69
   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.1
   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.83
   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
   OTHER INFORMATION: EST HUMAN HIT: AW452398.1, EVALUE 1.00e-49
    OTHER INFORMATION: SWISSPROT HIT: P32418, EVALUE 0.00e+00
US-09-864-761-33429
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 Best Local Similarity
                    69.3%; Pred. No. 8.5e-188;
 Matches 420; Conservative
                        76; Mismatches
                                       89;
                                           Indels
                                                  21;
                                                             8;
                                                      Gaps
         1 MAWLRLQPLTSAFLHFGLVTFVLF--LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
Qу
                     1:
                                            11:
                                                  1:11
Db
        11 MRRLSLSPTFSMGFHLLVTVSLLFSHVDHVIAETEMEGEGNETGE----CTGSYYCKKGV 66
        59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPN 118
Qy
           67 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN 126
Db
        119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM 178
Qу
           127 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 186
Db
        179 FIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL 238
Qу
           187 FIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF 246
Db
        239 FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH 295
Qу
           |||||:||: |||||:||||||::|:|| | | ||:||| |||
        247 FFFPICVVFAWVADRRLLFYKYVYKRYRAGKQRGMIIEHEGDRPSSKTEIEMDGKVVNSH 306
Db
        296 ---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 348
Qу
             307 VENFLDGALV-LEVDERDQDDEEARREMARILKELKOKHPDKEIEOLIELANYOVLSOOO 365
Db
        349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYOC 407
Qу
           366 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVTENDPVSKIFFEQGTYQC 425
Db
        408 LENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETOKEFSVG 467
Qу
           426 LENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGDTOKEIRVG 485
Db
        468 IIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
Qу
           1 1 11 1111 111
        486 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD 542
Db
        528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
Qу
                    543 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 602
Db
        588 EFKNDE 593
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RESULT 13

US-10-369-493-6319

[;] Sequence 6319, Application US/10369493

[;] Publication No. US20030233675A1

[;] GENERAL INFORMATION:

[;] APPLICANT: Cao, Yongwei

[;] APPLICANT: Hinkle, Gregory J.

```
APPLICANT: Goldman, Barry S.
  APPLICANT: Chen, Xianfeng
  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
OF
  TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
  FILE REFERENCE: 38-10(52052)B
  CURRENT APPLICATION NUMBER: US/10/369,493
  CURRENT FILING DATE: 2003-02-28
  PRIOR APPLICATION NUMBER: US 60/360,039
  PRIOR FILING DATE: 2002-02-21
  NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 6319
   LENGTH: 890
   TYPE: PRT
   ORGANISM: Caenorhabditis elegans
US-10-369-493-6319
                    41.8%; Score 2007; DB 15; Length 890;
 Query Match
 Best Local Similarity 45.9%; Pred. No. 5.9e-175;
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Qy
           Db
         1 MFLGISIVADRFMSSIEVITSMERTIVVKRPGLDPMAVOVRIWNDTVSNLTLMALGSSAP 60
Qy
        147 EILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFIT 206
                    Db
         61 EILLSIIEVIARGFEAGDLGPNTIVGSAAFNLFMIIAICVVVIPKGEIRROKHLDVFCVT 120
        207 AAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYR 266
Qу
           121 ATWSVFAYVWLYLILAFFSPGEIEIWEGALTFIFFPLTVFTAYMADIKLIONKFLPHRYR 180
Db
        267 TDKHRGIIIETEGDHPKGIÉMDGKMMNSHFLDGNLVPLEGKEVDESRREMIRILKDLKQK 326
Qу
             | | : | | | : | : |
                                    :|
                                           | :| |:| | :::::::
        181 RGSH-GQMIATEAEEMKMLE-----NGTQGDPALKAFEEHRQEFIELMREIRKQ 228
Db
        327 HPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKA-SSMSE 385
Qу
                229 NPHITPTELQKQAEYEMISRGPKSRAFYRVQATRRLIGGGDIVKKRIDKEHNKALDALVQ 288
Db
        386 VHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGAD 445
Qу
                   289 AQEKQSRDNTCKIFLDPAHYTVLESVGSFDVVVGRDGGPDGLTVMVDYFTEDGSANAGSD 348
Db
        446 YEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEG--MPPAIF 503
Qy
              349 YIPVKGTLTFYPEDKHQKVTIEVVDDDVFEEDEHFYLRLCNLRV---RTKDGIIIDPTRI 405
Dh
Qy
        504 NSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVI 563
             Dh
        406 GGLPV--AQLEMPNTATIMILDDDHAGVFGFEHDHFQVVENCGHLSLQMKRHSGARGKVI 463
        564 VPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKW 623
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Db
        464 IPFRTVEGTA-SADKHFEMKEGEIVFEDNQTEALVEIGIVDTEQYERSDYFYIELSPPIW 522
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APPLICANT: Slater, Steven C.

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624 -----LTMEEEEA 643
Qу
                             : | | | :: |
Db
        523 AKKMNDLSRIQERFORRMERKRGSSVASESKDSNTENALAPAEKSTRAASVDLLQPSSDP 582
        644 KR-----IAEMGKPVLGEHPKL 660
Qу
                                                   Db
         583 RRSSQTNSPHLTSRFRNRLGSWIAGMKGGNGDDEVTTSLTPSOLEIAEMGKPRLGEFTKC 642
         661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDED----ESGEE 716
Qy
            :: | || ||: ||::|| | :::|||||:||:||: ||:::
                                                            1 111
Db
        643 QITIRESKEFQGIVDRMIKNANTRIMLGTHSWREQFMEALVVSAGDDDDDEGEDGEDGEE 702
         717 R---LPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHF 773
Qу
               703 KEPEEPGCMDYVMHVLTVPWKLTFATIPPTDYFGGWATFVVAIFMIGVLTAVVGDLASQF 762
Db
         774 GCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLA 833
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            Db
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Qу
        834 WSVAAIYWALOGOEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKL 893
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US-10-243-552-971
; Sequence 971, Application US/10243552
; Publication No. US20030224379A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Zhiwei
  APPLICANT: Weng, Gezhi
  APPLICANT: Ma, Yunqing
  TITLE OF INVENTION: Novel Nucleic Acids and
  TITLE OF INVENTION: Polypeptides
  FILE REFERENCE: 807A
  CURRENT APPLICATION NUMBER: US/10/243,552
  CURRENT FILING DATE: 2002-09-12
  PRIOR APPLICATION NUMBER: US 60/322,511
  PRIOR FILING DATE: 2001-09-13
  PRIOR APPLICATION NUMBER: PCT/US00/35017
  PRIOR FILING DATE: 2000-12-22
  PRIOR APPLICATION NUMBER: US 09/488,725
  PRIOR FILING DATE: 2000-01-21
  PRIOR APPLICATION NUMBER: US 09/552,317
  PRIOR FILING DATE: 2000-04-25
  PRIOR APPLICATION NUMBER: PCT/US01/02623
  PRIOR FILING DATE: 2001-01-25
  PRIOR APPLICATION NUMBER: US 09/491,404
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PRIOR FILING DATE: 2000-01-25

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PRIOR APPLICATION NUMBER: PCT/US01/03800
  PRIOR FILING DATE: 2001-02-05
  PRIOR APPLICATION NUMBER: US 09/496,914
  PRIOR FILING DATE: 2000-02-03
  PRIOR APPLICATION NUMBER: US 09/560,875
  PRIOR FILING DATE: 2000-04-27
  PRIOR APPLICATION NUMBER: PCT/US01/04927
  PRIOR FILING DATE: 2001-02-26
  Remaining Prior Application data removed - See File Wrapper or PALM.
  NUMBER OF SEQ ID NOS: 998
  SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 971
   LENGTH: 394
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-243-552-971
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Qу
            | | : | | | : | : : | :
         18 RDGAVTPNRKNKGNYKKNPAKRCEASESSHGKVRSSSTCSVOLPOVKEALKTIHIKVIDD 77
Db
        606 EEYERQENFFIALGEPKWMERGI-SDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVII 664
Qу
            | ||: :|:|| : |: ::
                                 78 EAYEKNKNYFIEMMGPRMVDMSFQKDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVII 137
Db
        665 EESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDY 724
Qу
            138 EESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDY 197
Db
        725 VMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVT 784
Qу
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Db
        785 AVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQ 844
Qy
            258 AVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQ 317
Db
        845 GQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWL 904
Qу
            318 GQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWL 377
Db
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Qу
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Db
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US-10-369-493-6148
; Sequence 6148, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
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; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
OF
  TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
  FILE REFERENCE: 38-10(52052)B
  CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
  PRIOR APPLICATION NUMBER: US 60/360,039
  PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6148
  LENGTH: 807
   TYPE: PRT
  ORGANISM: Caenorhabditis elegans
US-10-369-493-6148
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Qy
           Db
         2 SSSANLTCKNGILI-----PALETTPRNAILYLAGLFYCFLGIAIAADIFMCSIEOIT 54
QУ
       107 SQEREVTIKKPNGETSTTT-----IRVWNETVSNLTLMALGSSAPEILLSLIEV 155
           Db
        55 SATKKVKKQKKAGQLVAKEEDEEIDEQYDYVRIWNPTVANLTLMALGSSAPEILLSIIEI 114
       ·156 CGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYI 215
Qу
            Db
       115 VGNGFKAGDLGPGTIVGSAAFNLFCISAICVFAV-GTQTKRIELYRVFVVTAFFGTFAYI 173
       216 WLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTD----- 268
Qу
           Db
       174 WVFLVLIVITPNVVDVWEAILTLLFFIILVVVSYAVDAQI-----WKKKKSSDLQEELEM 228
       269 -KHRGIIIETEGDHPKGIEMDGKMMNSHFL----DGNLVPLEGKEVDESRREMIRILKDL 323
Qу
           Db
       229 AQHDGKV----DDQPEKLSDEIKKWASNLSLNKEENDVIVDATPSVDTVR----RWTRSI 280
       324 KQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSM 383
Qу
             Db
       281 SHTYPSLSDEDQAKILAYRVSRTMSHDRLYYRIRAIRQLSSS---WRKSEEEEVLKMENO 337
       384 SEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAG 443
Qy
             338 ES--TDSASRRKTFVEFSARVYRVDATDETVSLKIERK-GNMESKFTVSYATVNGLAKKD 394
Db
Qу
       444 ADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEOPEEGMPPAIF 503
            :: | |: ||| | |: :|: : :: |:| | ::|:
       395 LNFLFKSETLQFNPGELHKTISIQLINAANWRPNDVFYVHLKIQDVDED----- 443
Db
       504 NSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH-VSESIGVMEVKVLRTSG-ARGT 561
Qу
                 444 -----SKICLGA-----CNVAHVVKENAGFSRSFVTRRGGKLKKP 478
Db
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Qу	562	VIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEP 621 : : : : : : :	-
Db	479	LQVHYETEDVTAKQGDDYTAVKDGILGFEGQEYEKYIDIDVIDDKMDEKDEAFIIELL 536	;
Qy	622	KWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIK 679)
Db	537	KVDEPGVSIGTRRKATITIISDDNVLKNITNVRKLMG 573	}
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Db	574	HYMRQLRPGKATWKEQILNAVSVNAGDLANATVSDCILHALAFPWKFAFAF 624	ı
Qу	740	VPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTF 799	į
Db	625	LPPPTIFYGYPCFVVALIGIGLVTAVVGDVASIFGCMVGLKDAVTAITLVALGTSLPDTF 684	:
Qу	800	ASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSV 859	į
Db	685	ASKIAAESDDTADNAVGNVTGSNSVNVFLGLGLPWVIASLYWASKGESFRVDAGDLGFSV 744	:
Qу	860	TLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAY 915	
Db	745	TVFMICSVLFLVVLVLRRKLKAFGQGELGGPFGTKTLSALFFVGLWIVYVGLSIWKMY 802	

Search completed: June 24, 2004, 16:17:29 Job time : 53.8014 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2004, 16:06:37; Search time 49.0084 Seconds

(without alignments)

5929.434 Million cell updates/sec

Title: US-10-054-680-2

Perfect score: 4797

1 MAWLRLQPLTSAFLHFGLVT.....LWLLYILFATLEAYCYIKGF 921 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

1017041 seqs, 315518202 residues Searched:

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SPTREMBL 25:* Database :

1: sp_archea:*

2: sp bacteria:*

3: sp_fungi:*

4: sp human:*

5: sp invertebrate:*

6: sp mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp phage:*

10: sp plant:*

11: sp rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:* 16: sp_bacteriap:*

17: sp archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result Query

No. Score Match Length DB ID

Description

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2	4692	97.8	921	11	Q7TS90	Q7ts90 mus musculu.
3	4671	97.4	925	4	Q96QG2	Q96qg2 homo sapien
4	4563.5	95.1	928	11	Q8VHJ8	Q8vhj8 mus musculu
5	4019	83.8	771	4	Q86Y47	Q86y47 homo sapien
6	3458.5	72.1	934	6	097801	097801 macaca mula
7	3442.5	71.8	941	6	Q28662	Q28662 oryctolagus
8	3437.5	71.7	941	6	Q9TS14	Q9ts14 oryctolagus
9	3427.5	71.5	934	11	Q9R238	Q9r238 rattus norv
10	3425.5	71.4	934	11	Q9WU30	Q9wu30 rattus norv
11	3417	71.2	957	11	Q9R239	Q9r239 rattus norv
12	3409.5	71.1	962	11	Q924Y2	Q924y2 rattus norv
13	3406	71.0	969	11	Q9WU29	Q9wu29 rattus norv
14	3357	70.0	921	11	Q8K596	Q8k596 mus musculu
15	3290.5	68.6	968	13	Q9PT19	Q9pt19 oncorhynchu
16	3229	67.3	963	13	Q7T3T7	Q7t3t7 oreochromis
17	3191.5	66.5	940	11	035157	035157 mus musculu
18	3012	62.8	595	11	Q9EPU8	Q9epu8 mus musculu
19	2896	60.4	607	11	Q8BXN1	Q8bxn1 mus musculu
20	2652	55.3	706	11	Q8BXB3	Q8bxb3 mus musculu
21	2533	52.8	892	5	002196	002196 loligo opal
22	2203.5	45.9	925	5	045630	O45630 caenorhabdi
23	2203.5	45.9	925	5	Q8MYP6	Q8myp6 caenorhabdi
24	2176.5	45.4	975	5	Q8MYP5	Q8myp5 caenorhabdi
25	2160.5	45.0	793	4	Q9H021	Q9h021 homo sapien
26	2156.5	45.0	602	6	Q9TV05	Q9tv05 macaca mula
27	2130.5	44.4	950	5	Q9VDG5	Q9vdg5 drosophila
28	2130.5	44.4	950	5	Q24413	Q24413 drosophila
29	2128.5	44.4	600	11	Q91ZJ7	Q91zj7 mus musculu
30	2126.5	44.3	600	11	Q9ET74	Q9et74 mus musculu
31	2119	44.2	950	5	018367	O18367 drosophila
32	2102	43.8	583	13	Q91850	Q91850 xenopus lae
33	2093.5	43.6	950	5	Q8I7I8	Q8i7i8 caenorhabdi
34	2001.5	41.7	880	5	Q21609	Q21609 caenorhabdi
35	1912.5	39.9	560	13	Q91849	Q91849 xenopus lae
36	1679	35.0	323	4	Q86TQ9	Q86tq9 homo sapien
37	1278	26.6	254	13	Q9YH83	Q9yh83 gallus gall
38	1192	24.8	807	5	Q21895	Q21895 caenorhabdi
39	1105.5	23.0	263	13	Q9YGE0	Q9yge0 oncorhynchu
40	1046.5	21.8	263	13	Q9YH84	Q9yh84 gallus gall
41	1038	21.6	264	13	Q9YGE1	Q9ygel oncorhynchu
42	970.5	20.2	267	13	Q9YGE2	Q9yge2 oncorhynchu
43	835	17.4	405	5	Q8I7I7	Q8i7i7 caenorhabdi
44	660	13.8	199	11	Q8R505	Q8r505 mus musculu
45	659	13.7	152	11	Q80XU9	Q80xu9 rattus sp.

ALIGNMENTS

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RESULT 1
Q96QG1
ID Q96QG1 PRELIMINARY; PRT; 924 AA.
AC Q96QG1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Sodium/calcium exchanger SCL8A3.
DE
GN
    SCL8A3.
OS
    Homo sapiens (Human).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    NCBI TaxID=9606;
OX
RN
    [1]
RP
    SEQUENCE FROM N.A.
RA
    Bortoluzzi S.;
RL
    Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN
RP
    SEQUENCE FROM N.A.
RA
    Gabellini N.;
RT
    "Characterization of the human SCL8A3 gene for solute carrier family
    8, member 3 (sodium/calcium exchanger).";
RT
    Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RL
    EMBL; AJ304853; CAC40985.1; -.
DR
DR
    GO; GO:0016021; C:integral to membrane; IEA.
    GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
    GO; GO:0006816; P:calcium ion transport; IEA.
DR
    InterPro; IPR003644; Calx beta.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
DR
    InterPro; IPRO04836; Na Ca Ex.
DR
    Pfam; PF03160; Calx-beta; 2.
DR
    Pfam; PF01699; Na Ca Ex; 2.
    PRINTS; PR01259; NACAEXCHNGR.
DR
    SMART; SM00237; Calx beta; 2.
DR
    TIGRFAMs; TIGR00845; caca; 1.
DR
             924 AA; 102694 MW; A0A556B753998A07 CRC64;
    SEQUENCE
SQ
                      99.4%; Score 4768.5; DB 4; Length 924;
 Query Match
 Best Local Similarity
                      99.4%; Pred. No. 0;
 Matches 918; Conservative
                            1; Mismatches
                                            2; Indels
                                                        3;
                                                           Gaps
                                                                  1;
          1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
Qу
            1 MAWLRLOPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGONNESCSGSSDCKEGVIL 60
Db
         61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPNGE 120
Qу
            61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPNGE 120
Db
        121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Qу
            Db
        121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
        181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qу
            181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Db
        241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qу
            241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Db
        301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Qу
            301 LVPLEGKEVDESRREMIRILKDLKOKHPEKDLDOLVEMANYYALSHQQKSRAFYRIQATR 360
Db
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Qу
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           361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Db
Qу
       421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
           421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Db
       481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qу
           481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Db
       541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Qy ·
           541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Db
       601 KIVDEEEYERQENFFIALGEPKWMERGISDV---TDRKLTMEEEEAKRIAEMGKPVLGEH 657
Qy
           601 KIVDEEEYEROENFFIALGEPKWMERGISALLLSPDRKLTMEEEEAKRIAEMGKPVLGEH 660
Db
       658 PKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEER 717
Qy
           661 PKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDOFMEAITVSAAGDEDEDESGEER 720
Db
       718 LPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTI 777
Qy
           Db
       721 LPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTI 780
       778 GLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVA 837
Qу
           781 GLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVA 840
Db
       838 AIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTW 897
Qу
           841 AIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTW 900
Db
       898 LFVSLWLLYILFATLEAYCYIKGF 921
Qy
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Db
       901 LFVSLWLLYILFATLEAYCYIKGF 924
RESULT 2
O7TS90
ID
   Q7TS90
             PRELIMINARY;
                           PRT:
                                 921 AA.
   O7TS90;
    01-OCT-2003 (TrEMBLrel. 25, Created)
DT
    01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE
    Slc8a3 protein.
OS
   Mus musculus (Mouse).
OC
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
   NCBI TaxID=10090;
RN
    [1]
RP
    SEQUENCE FROM N.A.
```

RC

STRAIN=C57BL/6; TISSUE=Brain;

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RX
    MEDLINE=22388257; PubMed=12477932;
RA
    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
    Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA
RA
    Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA
    Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA
    Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA
    Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA
    Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA
    Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA
    Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA
    Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
    Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA
    Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA
    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA
RA
    Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
    Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA
    Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA
RA
    Jones S.J., Marra M.A.;
RT
    "Generation and initial analysis of more than 15,000 full-length human
RT
    and mouse cDNA sequences.";
    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL
RN
    [2]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=C57BL/6; TISSUE=Brain;
    Strausberg R.;
RA
    Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RL
    EMBL; BC052435; AAH52435.1; -.
DR
    SEQUENCE 921 AA; 102376 MW;
                                50BCBD4DBE8A248A CRC64;
SQ
 Query Match
                       97.8%; Score 4692; DB 11;
                                                 Length 921;
                       97.6%; Pred. No. 0;
 Best Local Similarity
 Matches 899; Conservative
                             8; Mismatches
                                                           0;
                                                                      0;
                                             14;
                                                  Indels
                                                              Gaps
           1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
Qy
            1 MAWLRLQPLTSAFLHFGLVTFVLFLNCLRAEAGDSGDVPSAGQNNESCSGSSDCKEGVIL 60
Db
          61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPNGE 120
Qy
            61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Db
         121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Qу
            121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Db
         181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qу
            181 IIGICVYVIPDGETRKIKHLRVFFVTAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Db
         241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qу
             1114,11111,111,1111,1111,1111,111,1111,111,111,111,111,111,111,111,111,11
         241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Db
         301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Qу
              Db
         301 FTPLEGKEVDESRREMIRILKDLKOKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
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361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Qy
           361 MMTGAGNILKKHAAEOAKKTSSMSEVHTDEPEDFASKVFFDPCSYOCLENCGAVLLTVVR 420
Db
Qу
        421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
           421 KGGDISKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Db
        481 FVRLSNVRIEEEOPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qу
           481 FVRLSNVRVEEEQLAEGMLPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Db
       541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Qу
           541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDAYGELEFKNDETVKTIRV 600
Db
        601 KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL 660
Qу
           601 KIVDEEEYEROENFFIALGEPKWMERGISEVTDRKLTVEEEEAKRIAEMGKPVLGEHPKL 660
Db
        661 EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS 720
Qу
           661 EVIIEESYEFKSTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAGGDEDEDESGEERLPS 720
Db
       721 CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK 780
Qу
           721 CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFVVSILIIGMLTAIIGDLASHFGCTIGLK 780
Db
       781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840
Qу
           781 DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY 840
Db
        841 WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV 900
Qу
           841 WAMQGQEFHVSAGTLAFSVTLFTIFAFVCLSVLLYRRRPHLGGELGGPRGCKLATTWLFV 900
Db
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Qy
           1111111111111111111111
Db
        901 SLWLLYILFATLEAYCYIKGF 921
RESULT 3
0960G2
             PRELIMINARY;
                           PRT:
                                 925 AA.
ID
    Q96QG2
AC
    Q96QG2;
    01-DEC-2001 (TrEMBLrel. 19, Created)
דית
   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT
    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
    Sodium/calcium exchanger SCL8A3.
DE
GN
    SCL8A3.
OS
    Homo sapiens (Human).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX
   NCBI TaxID=9606;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RA
    Bortoluzzi S.;
```

```
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RL
RN
RP
    SEOUENCE FROM N.A.
    Gabellini N.;
RA
RT
    "Characterization of the human SCL8A3 gene for solute carrier family
RT
    8, member 3 (sodium/calcium exchanger).";
RL
    Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; AJ304852; CAC40984.1; -.
    GO; GO:0016021; C:integral to membrane; IEA.
DR
DR
    GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR
    GO; GO:0006816; P:calcium ion transport; IEA.
DR
    InterPro; IPR003644; Calx beta.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
    InterPro; IPR004836; Na Ca Ex.
    Pfam; PF03160; Calx-beta; 2.
DR
DR
    Pfam; PF01699; Na Ca Ex; 2.
DR
    PRINTS; PR01259; NACAEXCHNGR.
    SMART; SM00237; Calx_beta; 2.
DR
    TIGRFAMs; TIGRO0845; caca; 1.
DR
    SEOUENCE
             925 AA; 102803 MW; 0CCF8DA0881C4FDA CRC64;
SO
                     97.4%; Score 4671; DB 4; Length 925;
 Query Match
                     96.9%; Pred. No. 0;
 Best Local Similarity
 Matches 896; Conservative 11; Mismatches
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                                             Indels
                                                     4;
                                                         Gaps
                                                               1:
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Qу
           11||11||
Db
         1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
         61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Qу
           Db
         61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
        121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Qу
           Db
        121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
        181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qy
           181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVOVWEGLLTLFF 240
Db
        241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qy
           241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Db
        301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Qу
           Dh
        301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
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Qу
           Db
        361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
        421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETOKEFSVGIIDDDIFEEDEHF 480
Qу
           421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Db
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481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qy
            481 FVRLSNVRIEEEOPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Db
        541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Qy
            541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIHI 600
Db
Qy
        601 KIVDEEEYERQENFFIALGEPKWMERGISDV----TDRKLTMEEEEAKRIAEMGKPVLGE 656
            1::|:| ||: :|:|| : |: ::
                                            111111111111111111111111
        601 KVIDDEAYEKNKNYFIEMMGPRMVDMSFQKALLLSPDRKLTMEEEEAKRIAEMGKPVLGE 660
Db
        657 HPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDOFMEAITVSAAGDEDEDESGEE 716
Qу
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Db
        717 RLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCT 776
Qу
            721 RLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCT 780
Db
        777 IGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSV 836
Qу
            781 IGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSV 840
Db
        837 AAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATT 896
Qу
            Db
        841 AAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATT 900
        897 WLFVSLWLLYILFATLEAYCYIKGF 921
Qу
            Db
        901 WLFVSLWLLYILFATLEAYCYIKGF 925
RESULT 4
Q8VHJ8
ID
    O8VHJ8
              PRELIMINARY;
                              PRT;
                                    928 AA.
AC
    Q8VHJ8;
    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT
DT
DT
DE
    Sodium/calcium exchanger.
GN
    SLC8A3.
OS
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OC
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.

DR

DR

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       357 QATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLENCGAVL 415
Qy
           364 OATRLMTGAGNILKRHAADOARKAVSMHEVNTEMAENDPVSKIFFEOGTYOCLENCGTVA 423
Db
Qy
       416 LTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETOKEFSVGIIDDDIFE 475
           424 LTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETOKEIRVGIIDDDIFE 483
Db
       476 EDEHFFVRLSNVRIEEEOPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFE 535
Qy
          484 EDENFLVHLSNVKVSSETSEDGILEANHIS---TLACLGSPCTATVTIFDDDHAGIFTFE 540
Db
       536 CDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
Qу
              541 ESVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGELEFONDEIV 600
Db
       596 KTIRVKIVDEEEYEROENFFIALGEPKWMERG-----ISDVTDRK--LTMEE 640
Qу
           1:: | | | | :|
Db
       601 KIITIRIFDREEYEKECSLSLVLEEPKWIRRGMKALLLNELGGFTITEEYDDKQPLTSKE 660
       641 EEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDOFMEAI 700
Qу
           Db
       661 EEERRIAEMGRPILGEHTKLEVIIEESYEFKSTVDKLIKKTNLALVVGTNSWREOFIEAI 720
       701 TVSAAGDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIG 760
Qу
              Db
       721 TVSAGEDDDDDECGEEKLPSCFDYVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMIG 780
       761 MLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTG 820
Qу
           781 LLTAFIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTG 840
Db
       821 SNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPH 880
Qу
           841 SNAVNVFLGIGVAWSIAAIYHAANGEHFKVSPGTLAFSVTLFTIFAFINVGVLLYRRRPE 900
Db
       881 LGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
Qу
           Db
       901 IGGELGGPRTAKLLTSCLFVLLWLLYIFFSSLEAYCHIKGF 941
RESULT 8
09TS14
ID
   Q9TS14
             PRELIMINARY:
                           PRT:
                                941 AA.
AC
   Q9TS14;
DT
   01-MAY-2000 (TrEMBLrel. 13, Created)
   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DΤ
   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DΕ
   NA/CA exchanger isoform NACA6.
os
   Oryctolagus cuniculus (Rabbit).
OC
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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OX

NCBI TaxID=9986;

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RN
    [1]
    SEQUENCE FROM N.A.
RP
    MEDLINE=94148976; PubMed=8106495;
RX
    Kofuji P., Lederer W.J., Schulze D.H.;
RA
    "Mutually exclusive and cassette exons underlie alternatively spliced
RT
    isoforms of the Na/Ca exchanger.";
RT
    J. Biol. Chem. 269:5145-5149(1994).
RL
    PIR; B53335; B53335.
DR
DR
    GO; GO:0016021; C:integral to membrane; IEA.
    GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR
    GO; GO:0006816; P:calcium ion transport; IEA.
DR
DR
    InterPro; IPR003644; Calx beta.
    InterPro; IPR001623; DnaJ N.
DR
  InterPro; IPR004837; NaCa Exmemb.
    InterPro; IPR004836; Na Ca Ex.
DR
DR
    Pfam; PF03160; Calx-beta; 2.
DR
    Pfam; PF01699; Na Ca Ex; 2.
    PRINTS; PR01259; NACAEXCHNGR.
DR
    SMART; SM00237; Calx beta; 2.
DR
    TIGRFAMs; TIGR00845; caca; 1.
    PROSITE; PS50076; DNAJ 2; 1.
DR
    SEOUENCE
             941 AA; 104995 MW; AEC76774E9E81815 CRC64;
SO
                      71.7%; Score 3437.5; DB 6; Length 941;
 Query Match
 Best Local Similarity 71.0%; Pred. No. 4e-242;
 Matches 669; Conservative 111; Mismatches 125; Indels
                                                      37;
                                                                11;
                                                          Gaps
Qу
          8 PLTSAFLHFGLVTFVLF-LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPE 66
                         1::::
                                    |:
                                        ||:
                                              1:11 | 11:11|11|1 | 1:
                   : |
Db
          9 PFSMGFHLLAIVALFFFRVDHVSAETEMEGEGNETGE----CTGSYYCKKGVILPIWEPQ 64
         67 NPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPNGETSTTTI 126
Qу
            65 DPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKK-NGETTKTTV 123
Db
        127 RVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICV 186
Qу
            124 RIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIIALCV 183
Db
        187 YVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVOVWEGLLTLFFFPVCVL 246
Qу
            184 YVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVISPGIVEVWEGLLTFFFFPICVV 243
Db
        247 LAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH---FLDGN 300
Qу
             244 FAWVADRRLLFYKYVYKRYRAGKQRGMIIEHEGDRPSSKTEIEMDGKVVNSHVDNFLDGA 303
Db
        301 LVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRI 356
Qу
                       Db
        304 LV-LDVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQKSRAFYRI 362
        357 QATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLENCGAVL 415
Qу
            363 OATRLMTGAGNILKRHAADQARKAVSMHEVNTEMAENDPVSKIFFEQGTYQCLENCGTVA 422
Db
        416 LTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFE 475
Qу
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Db
        423 LTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVGIIDDDIFE 482
        476 EDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFE 535
Qу
            483 EDENFLVHLSNVKVSSETSEDGILEANHIS---TLACLGSPCTATVTIFDDDHAGIFTFE 539
Db
        536 CDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
Qv
               540 ESVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGELEFONDEIV 599
Db
        596 KTIRVKIVDEEEYEROENFFIALGEPKWMERG-----ISDVTDRK--LTME 639
Qy
            1:: | | | :
        600 KTISVKVIDDEEYEKNKTFFLEIGEPRLVEMSEKKALLLNELGGFTITEEYDDKOPLTSK 659
Db
        640 EEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEA 699
Qу
            660 EEEERRIAEMGRPILGEHTKLEVIIEESYEFKSTVDKLIKKTNLALVVGTNSWREQFIEA 719
Db
        700 ITVSAAGDEDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILII 759
Qу
                 720 ITVSAGEDDDDDECGEEKLPSCFDYVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMI 779
Db
Qу
        760 GMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALODVYADASIGNVT 819
            Db
        780 GLLTAFIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTFASKVAATODOYADASIGNVT 839
        820 GSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRP 879
Qу
            Db
        840 GSNAVNVFLGIGVAWSIAAIYHAANGEHFKVSPGTLAFSVTLFTIFAFINVGVLLYRRRP 899
        880 HLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
Qу
            Db
        900 EIGGELGGPRTAKLLTSCLFVLLWLLYIFFSSLEAYCHIKGF 941
RESULT 9
Q9R238
ID
    09R238
              PRELIMINARY:
                             PRT:
                                   934 AA.
AC
    Q9R238;
    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
DT
    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT
DE
    Na+/Ca2+-exchanging protein.
os
    Rattus norvegicus (Rat).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX
    NCBI TaxID=10116;
RN
    [1]
    SEQUENCE FROM N.A.
RP
RC
    STRAIN=Dahl/Rapp R Sprague-Dawley;
RA
    Unlap M.T., Bell P.D.;
RT
    "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
RT
    Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RL
    Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; AF109163; AAD23386.1; -.
DR
    GO; GO:0016021; C:integral to membrane; IEA.
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GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.

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GO; GO:0006816; P:calcium ion transport; IEA.
    InterPro; IPR003644; Calx beta.
DR
    InterPro; IPR001623; DnaJ N.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
    InterPro; IPR004836; Na Ca Ex.
DR
    Pfam; PF03160; Calx-beta; 2.
DR
    Pfam; PF01699; Na Ca Ex; 2.
DR
    PRINTS; PR01259; NACAEXCHNGR.
DR
DR
    SMART; SM00237; Calx beta; 2.
    TIGRFAMs; TIGR00845; caca; 1.
DR
    PROSITE; PS50076; DNAJ 2; 1.
DR
    SEQUENCE
            934 AA; 104166 MW; C04E0D8A75633DDC CRC64;
SQ
 Query Match
                    71.5%; Score 3427.5; DB 11; Length 934;
                    70.9%; Pred. No. 2.1e-241;
 Best Local Similarity
 Matches 671; Conservative 107; Mismatches 127; Indels
                                                   41; Gaps
                                                             11;
         4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK 55
Qy
                : : | | | | | |
                                      11 11:
         2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN----ETTECTGSYYCK 53
Db
        56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
Qy
           54 KGVILPIWEPODPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK 113
Db
        116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 175
Qу
           Db
        114 KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA 173
        176 FNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL 235
Qу
           174 FNMFIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL 233
Db
        236 LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMM 292
Qу
           Db
        234 LTFFFFPICVVFAWVADRRLLFYKYVYKRYRAGKQRGMIIEHEGDRPASKTEIEMDGKVV 293
        293 NSH---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS 345
Qy
                Db
        294 NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS 352
        346 HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
Qу
            Db
        353 OOOKSRAFYRIOATRLMTGAGNILKRHAADOARKAVSMHEVNMDVVENDPVSKVFFEOGT 412
        405 YQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
Qу
           413 YOCLENCGTVALTIIRRGGDLTNTVSVDFRTEDGTANAGSDYEFTEGTVIFKPGETOKEI 472
Db
        465 SVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
Qy
            Db
        473 RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528
        524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
Qу
                        529 FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588
Db
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DR

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584 YGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERGI-----SDVTDRK- 635
Qy
             : |::
        589 CGELEFONDEIVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKGGFTLTEEYDDKQP 648
Db
        636 LTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQ 695
Qy
            649 LTSKEEEERRIAEMGRPILGEHTKLEVIIEESYEFKSTVDKLIKKTNLALVVGTNSWREO 708
Db
Qу
        696 FMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVS 755
            709 FIEAITVSAGEDDDDDECGEEKLPSCFDYVMHFLTVFWKVLFAFVPPTEYWNGWACFIVS 768
Db
        756 ILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASI 815
Qу
           769 ILMIGLLTAFIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTFASKVAATQDQYADASI 828
Db
        816 GNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLY 875
Qу
            829 GNVTGSNAVNVFLGIGVAWSIAAIYHAANGEQFKVSPGTLAFSVTLFTIFAFINVGVLLY 888
Db
        876 RRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
Qу
            889 RRRPEIGGELGGPRTAKLLTSSLFVLLWLLYIFFSSLEAYCHIKGF 934
Db
RESULT 10
O9WU30
ID
    Q9WU30
              PRELIMINARY;
                              PRT:
                                    934 AA.
AC
    09WU30;
DT
    01-NOV-1999 (TrEMBLrel. 12, Created)
    01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT
    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT
DΕ
    Na+/Ca2+-exchanging protein.
    Rattus norvegicus (Rat).
os
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX
    NCBI TaxID=10116;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=Sprague-Dawley;
RA
    Unlap M.T., Bell P.D.;
    "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
RT
    Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RT
RL
    Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; AF109166; AAD23389.1; -.
    GO; GO:0016021; C:integral to membrane; IEA.
DR
    GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR
DR
    GO; GO:0006816; P:calcium ion transport; IEA.
DR
    InterPro; IPR003644; Calx beta.
DR
    InterPro; IPR001623; DnaJ N.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
    InterPro; IPR004836; Na Ca Ex.
DR
    Pfam; PF03160; Calx-beta; 2.
DR
    Pfam; PF01699; Na Ca Ex; 2.
DR
    PRINTS; PR01259; NACAEXCHNGR.
DR
    SMART; SM00237; Calx beta; 2.
DR
    TIGRFAMs; TIGRO0845; caca; 1.
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DR PROSITE; PS50076; DNAJ_2; 1.
SQ SEQUENCE 934 AA; 104210 MW; 054D06E9179098B5 CRC64;

Query Match 71.4%; Score 3425.5; DB 11; Length 934; Best Local Similarity 70.8%; Pred. No. 2.9e-241; Matches 670; Conservative 108; Mismatches 127; Indels 41; Gaps 11; 4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK 55 Qу : : | | | | | .11 11: 1:11 11 2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53 Db 56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115 Qу 54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK 113-Db 116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 175 Qу 114 KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILPSVIEVCGHNFTAGDLGPSTIVGSAA 173 Db 176 FNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL 235 Qу 174 FNMFIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL 233 Db 236 LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMM 292 Qу 234 LTFFFFPICVVFAWVADRRLLFYKYVYKRYRAGKQRGMIIEHEGDRPASKTEIEMDGKVV 293 Db 293 NSH---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS 345 Qу 294 NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS 352 Db 346 HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404 Qу 353 QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412 Db 405 YQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464 Qу 413 YOCLENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472 Db 465 SVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523 Qу | :| : 473 RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528 Db 524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583 Qу 1111111111 529 FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588 Db 584 YGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERGI----SDVTDRK- 635 Qу 589 CGELEFONDEIVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKGGFTLTEEYDDKQP 648 Db 636 LTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQ 695 Qу 649 LTSKEEEERRIAEMGRPILGEHTKLEVIIEESYEFKSTVDKLIKKTNLALVVGTNSWREQ 708 Db 696 FMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVS 755 Qу

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709 FIEAITVSAGEDDDDDECGEEKLPSCFDYVMHFLTVFWKVLFAFVPPTEYWNGWACFIVS 768
Db
         756 ILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASI 815
Qy
             769 ILMIGLLTAFIGDLASHFGCTIGLKDSVTAVVFVALGTSVPDTFASKVAATQDQYADASI 828
Db
         816 GNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLY 875
Qy
             829 GNVTGSNAVNVFLGIGVAWSIAAIYHAANGEQFKVSPGTLAFSVTLFTIFAFINVGVLLY 888
Db
         876 RRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
Qу
             Db
         889 RRRPEIGGELGGPRTAKLLTSSLFVLLWLLYIFFSSLEAYCHIKGF 934
RESULT 11
Q9R239
ID
    Q9R239
               PRELIMINARY; PRT;
                                      957 AA.
АÇ
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DT
    01-MAY-2000 (TrEMBLrel. 13, Created)
    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE
    Na+/Ca2+-exchanging protein.
os
    Rattus norvegicus (Rat).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX
    NCBI TaxID=10116;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=Dahl/Rapp S Sprague-Dawley;
RA
    Unlap M.T., Bell P.D.;
RT
    "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
    Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RT
RL
    Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; AF109164; AAD23387.1; -.
DR
    GO; GO:0016021; C:integral to membrane; IEA.
    GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR
    GO; GO:0006816; P:calcium ion transport; IEA.
DR
DR
    InterPro; IPR003644; Calx beta.
DR
    InterPro; IPR001623; DnaJ N.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
    InterPro; IPRO04836; Na Ca Ex.
DR
    Pfam; PF03160; Calx-beta; 2.
DR
    Pfam; PF01699; Na Ca Ex; 2.
DR
    PRINTS; PR01259; NACAEXCHNGR.
    SMART; SM00237; Calx beta; 2.
DR
DR
    TIGRFAMs; TIGR00845; caca; 1.
DR
    PROSITE; PS50076; DNAJ 2; 1.
SQ
    SEQUENCE 957 AA; 106724 MW; 7A146630451EAA7E CRC64;
 Query Match
                       71.2%; Score 3417; DB 11; Length 957;
 Best Local Similarity 69.5%; Pred. No. 1.3e-240;
 Matches 673; Conservative 104; Mismatches 128; Indels
                                                           64; Gaps
                                                                      11;
           4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK 55
Qу
                  : : | | | | | |
                                            11-11:
           2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53
Db
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Qy	56	EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK : :	115
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK	113
Qу	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA	175
Db	114	: : :	173
Qy	176	FNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL	235
Db	174	: :	233
Qy	236	LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMM	292
Db	234	: : : : : :	293
Qy	293	NSHFLDGNLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS	345
Db	294		352
Qу	346	HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT	412
Qу	405	YQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
Db	413	YQCLENCGTVALTIIRRGGDLTNTVSVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qу	465	SVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
Db	473	RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDGILDSNHVSAIACLGSPNTATITI	528
Qу	524	LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT	583
Db	529	FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT	588
QУ	584	YGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG	627
Db	589	CGELEFQNDEIVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKGGFTLTGQPVFRKV	648
Qy	628	ISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKT	672
Db	649	HARDHPIPSTVISISEEYDDKQPLTSKEEEERRIAEMGRPILGEHTKLEVIIEESYEFKS	708
Qy	673	TVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVF	732
Db	709	TVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKLPSCFDYVMHFLTVF	768
Qу	733	WKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFG	792
Db	769	WKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSVTAVVFVALG	828
Qy	793	TSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSA	852
Db	829	TSVPDTFASKVAATODOYADASTGNVTGSNAVNVFLGTGVAWSTAATYHAANGEOFKVSP	888

```
853 GTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATL 912
Qу
             889 GTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSSLFVLLWLLYIFFSSL 948
Db
         913 EAYCYIKGF 921
Qу
             1111:111
         949 EAYCHIKGF 957
Db
RESULT 12
0924Y2
ID
    O924Y2
               PRELIMINARY; PRT;
                                       962 AA.
AC
    Q924Y2;
DT
    01-DEC-2001 (TrEMBLrel. 19, Created)
    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT
DE
    Na+/Ca2+ exchanger.
OS
    Rattus norvegicus (Rat).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC
OX
    NCBI TaxID=10116;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=Sprague-Dawley;
    Unlap M.T., Bell P.D., Williams I.;
RA
RT
    "Cloning and expression of a mesangial cell Na+/Ca2+ exchanger from
RT
    Sprague-Dawley rats.";
RL
    Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; AY033398; AAK52307.1; -.
DR
    GO; GO:0016021; C:integral to membrane; IEA.
    GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR
DR
    GO; GO:0006816; P:calcium ion transport; IEA.
DR
    InterPro; IPR003644; Calx beta.
DR
    InterPro; IPRO01623; DnaJ N.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
    InterPro; IPRO04836; Na Ca Ex.
DR
    Pfam; PF03160; Calx-beta; 2.
    Pfam; PF01699; Na Ca Ex; 2.
DR
DR
    PRINTS; PR01259; NACAEXCHNGR.
DR
    SMART; SM00237; Calx beta; 2.
DR
    TIGRFAMs; TIGR00845; caca; 1.
    PROSITE; PS50076; DNAJ 2; 1.
DR
    SEQUENCE 962 AA; 107270 MW; 1AA422ED25964182 CRC64;
SQ
 Query Match
                        71.1%; Score 3409.5; DB 11; Length 962;
 Best Local Similarity 69.0%; Pred. No. 4.6e-240;
 Matches 672; Conservative 105; Mismatches 128; Indels
                                                           69; Gaps
                                                                      11;
           4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK 55
Qу
                  : : | | | | | |
                                           11 11:
Db
           2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53
Qу
          56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
             Db
          54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK 113
Qу
         116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 175
```

Db	114	: : :
Qy	176	FNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL 235
Db	174	: :
Qy	236	LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMM 292
Db	234	: : : : :
Qу	293	NSHFLDGNLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS 345
Db .	294	NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS 3.52.
Qy	346	HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412
Qy	405	YQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
Db	413	YQCLENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472
Qy	465	SVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
Db	473	RVGIIDDDIFEEDENFLVHLSNVRVSSGVSEDGILDSNHVSAIACLGSPNTATITI 528
Qy	524	LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
Db	529	FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588
Qу	584	YGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG 627
Db	589	CGELEFQNDEIVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKGGFTLTGKKMYGQP 648
Qу	628	ISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEES 667
Db	649	VFRKVHARDHPIPSTVISISEEYDDKQPLTSKEEEERRIAEMGRPILGEHTKLEVIIEES 708
Qу	668	YEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMH 727
Db	709	YEFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKLPSCFDYVMH 768
Qу	728	FLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVV 787
Db	769	FLTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSVTAVV 828
Qу	788	FVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQE 847
Db	829	FVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAANGEQ 888
Qу	848	FHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYI 907
Db	889	FKVSPGTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSSLFVLLWLLYI 948
Qу	908	LFATLEAYCYIKGF 921 :: :

```
RESULT 13
09WU29
    09WU29
               PRELIMINARY; PRT; 969 AA.
ID
AC
    09WU29;
DT
    01-NOV-1999 (TrEMBLrel. 12, Created)
    01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT
DT
DE
    Na+/Ca2+-exchanging protein.
os
    Rattus norvegicus (Rat).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC
OX
    NCBI TaxID=10116;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=Spraque-Dawley;
RA
    Unlap M.T., Bell P.D.;
RT
    "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
RT
    Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RL
    Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; AF109165; AAD23388.1; -.
DR
    GO; GO:0016021; C:integral to membrane; IEA.
DR
    GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR
    GO; GO:0006816; P:calcium ion transport; IEA.
DR
    InterPro; IPR003644; Calx beta.
DR
    InterPro; IPR001623; DnaJ N.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
    InterPro; IPR004836; Na Ca Ex.
DR
    Pfam; PF03160; Calx-beta; 2.
DR
    Pfam; PF01699; Na Ca Ex; 2.
    PRINTS; PR01259; NACAEXCHNGR.
DR
    SMART; SM00237; Calx beta; 2.
DR
DR
    TIGRFAMs; TIGR00845; caca; 1.
DR
    PROSITE; PS50076; DNAJ 2; 1.
    SEQUENCE 969 AA; 108037 MW; 1D64F6073D3C9CF5 CRC64;
SO
 Query Match 71.0%; Score 3406; DB 11; Length 969; Best Local Similarity 68.5%; Pred. No. 8.3e-240;
 Matches 672; Conservative 105; Mismatches 128; Indels 76; Gaps
                                                                       11;
           4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGONNESCSGSSDCK 55
Qу
                   : : | | | | |
                                            11 11:
                                                             1:11
Db
           2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53
          56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIK 115
Qу
             Db
          54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK 113
Qу
         116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 175
             Db
         114 KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILPSVIEVCGHNFTAGDLGPSTIVGSAA 173
         176 FNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVOVWEGL 235
Qу
             Db
         174 FNMFIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL 233
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ΟÀ	236		292
Db	234	LTFFFFPICVVFAWVADRRLLFYKYVYKRYRAGKQRGMIIEHEGDRPASKTEIEMDGKVV	293
QУ	293	NSHFLDGNLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS	345
Db	294	NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qу	346	HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT	412
Qy	4.05	YQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	4.64.
Db	413	YQCLENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qy	465	SVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
Db	473	RVGIIDDDIFEEDENFLVHLSNVRVSSGVSEDGILDSNHVSAIACLGSPNTATITI	528
Qу	524	LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT	583
Db	529	FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT	588
Qу	584	YGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG	627
Db	589	CGELEFQNDEIVKIITIRIFDREEYEKECSFSLVLEEPKWIRRGMKALLLNELGGFTLTG	648
Qу	628	ISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKL	660
Db	649	KKMYGQPVFRKVHARDHPIPSTVISISEEYDDKQPLTSKEEEERRIAEMGRPILGEHTKL	708
Qу	661	EVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPS	720
Db	709	EVIIEESYEFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKLPS	768
Qу	721	CFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLK	780
Db	769	CFDYVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLK	828
Qу	781	DSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIY	840
Db	829	DSVTAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIY	888
Qy	841	WALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFV	900
Db	889	HAANGEQFKVSPGTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSSLFV	948
Qy	901	SLWLLYILFATLEAYCYIKGF 921	
Db	949	LLWLLYIFFSSLEAYCHIKGF 969	

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AC
    Q8K596;
    01-OCT-2002 (TrEMBLrel. 22, Created)
DT
    01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT
    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT
DE
    Sodium-calcium exchanger.
GN
    SLC8A2.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=Cerebellum;
RA
    Kraev A.;
RT
    "Towards a complete inventory of calcium transporters of the house
RT
    mouse.";
RL
    Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; AF503502; AAM22231.1; -.
DR
    MGD; MGI:107996; Slc8a2.
    GO; GO:0016021; C:integral to membrane; IEA.
DR
    GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR
    GO; GO:0006816; P:calcium ion transport; IEA.
DR
DR
    InterPro; IPR003644; Calx beta.
DR
    InterPro; IPR004837; NaCa Exmemb.
    InterPro; IPR004836; Na Ca Ex.
DR
    Pfam; PF03160; Calx-beta; 2.
DR
    Pfam; PF01699; Na Ca Ex; 2.
DR
    PRINTS; PR01259; NACAEXCHNGR.
DR
    SMART; SM00237; Calx beta; 2.
DR
    TIGRFAMs; TIGR00845; caca; 1.
SQ
    SEQUENCE 921 AA; 100711 MW; 5F5A378FF982073D CRC64;
                       70.0%; Score 3357; DB 11; Length 921;
 Query Match
 Best Local Similarity 69.3%; Pred. No. 2.9e-236;
 Matches 633; Conservative 133; Mismatches 113; Indels
                                                         34; Gaps
                                                                     9;
         31 EAGGSGDVPSTGQNN-----ESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALI 85
Qу
            21 EATPTPSLPPPTANDSDASPEGCQGSYRCQPGVLLPVWEPEDPSLGDKVARAVVYFVAMV 80
Db
         86 YMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSA 145
Qу
            81 YMFLGVSIIADRFMASIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSA 140
Db
         146 PEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFI 205
Qу
            141 PEILLTVIEVCGHNFQAGELGPGTIVGSAAFNMFVVIAVCVYVIPAGESRKIKHLRVFFV 200
Db
         206 TAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKY 265
Qу
            Db
         201 TASWSIFAYVWLYLILAVFSPGVVQVWEALLTLIFFPVCVVFAWMADKRLLFYKYVYKRY 260
         266 RTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGNL----VPLEGKEVDESRREMIRIL 320
Qу
                 1111 111 11 11:11 :: : 1 1
                                                 | | | :|:| |||:|:|:
         261 RTDPRSGIIIGAEGDPPKSIELDGTFVGTE-VPGELGALGTGPAEARELDASRREVIQIL 319
Db
         321 KDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKA 380
Qу
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320 KDLKQKHPDKDLEQLMGIAKYYALLHQQKSRAFYRIQATRLMTGAGNVLRRHAADAARRP 379
Db
        381 SSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSA 440
Qу
                  Db
        380 GATDGAPDDE-DDGASRIFFEPSLYHCLENCGSVLLSVACOGGEGNSTFYVDYRTEDGSA 438
Qу
        441 NAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEO----PEE 496
            439 KAGSDYEYSEGTLVFKPGETQKDLRIGIIDDDIFEEDEHFFVRLLNLRVGDAQGMFEPDG 498
Db
        497 GMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTS 556
Qу
                     -:|||| :| ::|:|:|:|
           1
Db
        499 G-----GRPKGRLVAPLLATVTILDDDHAGIFSFQDRLLHVSECMGTVDVRVVRSS 549
        557 GARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYEROENFFI 616
Qy
           550 GARGTVRLPYRTVDGTARGGGVHYEDACGELEFGDDETMKTLQVKIVDDEEYEKKDNFFI 609
Db
        617 ALGEPKWMERGISDVT-----DRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEF 670
QУ
                             1:1:1 1:111:1111111111: :1111111:1
            ||:|:|::|||
        610 ELGQPQWLKRGISALLLNQGNGDKKITAEQEEAQRIAEMGKPVLGENNRLEVIIEESYDF 669
Db
        671 KTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG--EERLPSCFDYVMHF 728
Qу
           670 KNTVDKLIKKTNLALVIGTHSWREQFIEAVTVS-AGDEEEDEDGPREERLPSCFDYVMHF 728
Db
        729 LTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVF 788
Qу
           729 LTVFWKVLFACVPPTEYCNGWACFGVCILVIGVLTALIGDLASHFGCTVGLKDSVNAVVF 788
Db
        789 VAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEF 848
Qу
           789 VALGTSIPDTFASKVAALQDQCADASIGNVTGSNAVNVFLGLGVAWSVAAVYWAVQGRPF 848
Db
        849 HVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYIL 908
Qy
            849 EVRAGTLAFSVTLFTVFAFVCIAVLLYRRRPQIGGELGGPRGPKLATTALFLGLWFLYIL 908
Db
        909 FATLEAYCYIKGF 921
Qy
           1::|||||:|:||
        909 FSSLEAYCHIRGF 921
Db
RESULT 15
09PT19
ID
    09PT19
             PRELIMINARY;
                            PRT;
                                  968 AA.
AC
    O9PT19;
DT
    01-MAY-2000 (TrEMBLrel. 13, Created)
DT
    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE
    Cardiac sodium-calcium exchanger.
GN
os
    Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Actinopterygii; Neopterygii; Teleostei; Euteleostei;
```

Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OC

```
NCBI TaxID=8022;
OX
RN
    [1]
    SEQUENCE FROM N.A.
RP
    TISSUE=Heart;
RC
    MEDLINE=99447215; PubMed=10516099;
RX
    Xue X.H., Hryshko L.V., Nicoll D.A., Philipson K.D., Tibbits G.F.;
RA
RT
    "Cloning, expression, and characterization of the trout cardiac
RT
    Na(+)/Ca(2+) exchanger.";
RL
    Am. J. Physiol. 277:C693-C700(1999).
    EMBL; AF175313; AAF06363.1; -.
DR
DR
    GO; GO:0016021; C:integral to membrane; IEA.
    GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR
DR
    GO; GO:0006816; P:calcium ion transport; IEA.
DR
    InterPro; IPR003644; Calx beta.
    InterPro; IPR004837; NaCa Exmemb.
DR
    InterPro; IPRO04836; Na Ca Ex.
DR
    Pfam; PF03160; Calx-beta; 2.
DR
    Pfam; PF01699; Na Ca Ex; 2.
DR
    PRINTS; PR01259; NACAEXCHNGR.
DR
    SMART; SM00237; Calx beta; 2.
DR
DR
    TIGRFAMs; TIGR00845; caca; 1.
SO
    SEQUENCE 968 AA; 107504 MW; 5F8A92824B26DA36 CRC64;
 Query Match 68.6%; Score 3290.5; DB 13; Length 968; Best Local Similarity 66.5%; Pred. No. 2.3e-231;
 Matches 640; Conservative 120; Mismatches 132; Indels
                                                        70; Gaps
                                                                  13;
         19 VTFVLFLNGLRAEAGGSGDVPSTG-----ONNESC-SGSSDCKEGVILPIWYPENPSL 70
Qу
                        1: : | | |
                                      18 VLLAVFSSEIKFVTAGNSN-PSLGTNSSIGNOTNKKCDSVDTECKVGVILPIWLPENTSF 76
         71 GDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPNGETSTTTIRVWN 130
Qу
            77 GDKLARATVYFVALFYMFLGVSIIADRFMASIEVITSOEREITIKKPNGEKVTTTVRIWN 136
Db
        131 ETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIP 190
Qy
            137 ETVSNLTLMALGSSAPEILLSVVEVCGHNFDAGDLGPNTIVGSAAFNMFVIIGFCVSVIP 196
Db
        191 DGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWV 250
Qу
            111 | 11:1111111:11 | 111111 | 111:111 | 111:111111:111111:11:11:11:11
Db
        197 DGEHRKVKHLRVFFVTATWSIFAYTWLYLILAVISPGIVQVWEGLVTLFFFPLCVGMAYV 256
        251 ADKRLLFYKYMHKKYRTDKHRGIIIETEGD----HPKGIEMDGKMMNSH-FLDGNLVPLE 305
Qy
            1111111:11 1:11 : :
Db
        257 ADRRLLVYKYMYKRYRAGKRRGVIIETEGEAQIPSKMDIEMDGKMLNSESFMDG-AMGFD 315
Qy
        306 GKEVD--ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHOOKSRAFYRIOATRMMT 363
             316 EKDLDEEEARREMVRILKELKQKHPEKETEQLIELANYQVLTQQQKSRAFYRCQATRIMT 375
Db
Qy
        364 GAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYOCLENCGAVLLTVVRKG 422
            Db
        376 GAGNVLKKHAADQARKAVGAYEIRSEVSENDFSSKVFFDPGTYQCLENCGTVALNVVRLG 435
        423 GDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHFFV 482
ÒУ
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Db	436	GDLTNTVSVEYRTEDGTANAGSDYQFTEGVVVFNPGETEKEIRIDIIDDDIFEEDEHFLV	495
Qу	483	RLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVS	542
Db	496	HLSNVKVISEGTGYVQPRANHLD-TLAGLGLPCSATVTIFDDDHAGIFTFEEPVMTIS	552
Qу	543	ESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKI	602
Db	553	ESIGMMEVKVLRTSGARGLVVVPYKTMEGTAKGGGEDFEDTHGALEFQNDEIFKSIQINI	612
Qy	603	VDEEEYERQENFFIALGEPKWMERGISDVTDRK	635
Db	613	IDDEEYEKNKNFFLEMGEPQLLEMSERKAVLLQEIGGFVKTGRDVYRKVQGRDNP	667
Qy	636	LTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIK	679
Db	668	VPATIISLAEEGDEEALSKKEEEERRIAEMGRPTLGEHVKLEVVIEESYEFKNTVDKLIK	727
Qy	680	KTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVFWKVLFAC	739
Db	728	KTNLALLIGTNSWRQQFMEAITVS-SGDDDEDECGEEKLPSCFDYVMHFLTVFWKLLFAF	786
Qy	740	VPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTF	799
Db	787	VPPTDYWNGWACFVVSISMIGLLTAFIGDLASHFGCTVGLKDSVTAVVFVALGTSVPDTF	846
Qy	800	ASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSV	859
Db	847	ASKVAAIQDQYADAFIGNVTGSNAVNVFLGIGVAWSIAAIYHNSKGNDFRVDPGTLAFSV	906
Qy	860	TLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIK	919
Db	907	TLFTIFAFVAVAVLMYRRRPEIGGELGGPRGPKIATTCLFFSLWLMYIVFSSLEAYCHVK	966
Qy	920	GF 921	
Db	967	GF 968	

Search completed: June 24, 2004, 16:14:13 Job time: 53.0084 secs

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OM protein - protein search, using sw model

Run on: June 24, 2004, 15:55:42; Search time 17.3323 Seconds

(without alignments)

2766.900 Million cell updates/sec

Title: US-10-054-680-2

Perfect score: 4797

Sequence: 1 MAWLRLQPLTSAFLHFGLVT.....LWLLYILFATLEAYCYIKGF 921

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt 42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			8				
Re	sult		Query				
_	No.	Score	Match	Length	DB	ID	Description
	1	4784	99.7	927	1	NAC3_HUMAN	P57103 homo sapien
	2	4686	97.7	927	1	NAC3 RAT	P70549 rattus norv
	3	3447.5	71.9	970	1	NAC1 CANFA	P23685 canis famil
	4	3442.5	71.8	970	1	NAC1 FELCA	P48767 felis silve
	5	3439.5	71.7	973	1	NAC1 HUMAN	P32418 homo sapien
	6	3432.5	71.6	970	1	NAC1 CAVPO	P48766 cavia porce
	7	3428	71.5	971	1	NAC1_RAT	Q01728 rattus norv
	8	3425.5	71.4	970	. 1	NAC1_BOVIN	P48765 bos taurus
	9	3405.5	71.0	970	1	NAC1 MOUSE	P70414 mus musculu
	10	3373.5	70.3	921	1	NAC2_HUMAN	Q9upr5 homo sapien
	11	3357	70.0	921	1	NAC2_RAT	P48768 rattus norv
	12	306.5	6.4	1216	1	NKX1_BOVIN	Q28139 bos taurus
	13	303.5	6.3	1181	1	NKX1_RAT	Q9qzm6 rattus norv
	14	293	6.1	1099	1	NKX1 HUMAN	060721 homo sapien
	15	266	5.5	645	1	NKX3 MOUSE	Q99pd7 mus musculu
	16	262.5	5.5	624	1	NKX3_RAT	Q9epq0 rattus norv
	17	258.5	5.4	644	1	NKX3_HUMAN	Q9hc58 homo sapien
			0		_		Zonece neme supi

18 251 5.2 663 1 NKX1_CHICK Q9ial8 gallus 19 247 5.1 605 1 NKX4_HUMAN Q8cgq8 mus mu 20 246 5.1 605 1 NKX4_HUMAN Q9ui40 homo s 21 239.5 5.0 661 1 NKX2_HUMAN Q9ui40 homo s 22 231.5 4.8 856 1 NCKX_DROME Q9u6a0 drosop 23 227 4.7 670 1 NKX2_RAT O54701 rattus 24 216.5 4.5 651 1 NKX2_CHICK Q9ia17 gallus 25 147 3.1 590 1 YKTA_CAEEL P34322 caenor 26 143.5 3.0 325 1 YRBG_ECOLI P45394 escher. 27 142.5 3.0 302 1 Y991_METJA Q57556 methan 28 142 3.0 302 1 Y991_METJA Q57556 methan 29 141.5	18	251	5.2	663	1	NKX1 CHICK	00:010	~~11ua ~~11
20 246 5.1 605 1 NKX4_MOUSE Q8cgq8 mus mu 21 239.5 5.0 661 1 NKX2_HUMAN Q9ui40 homo s 22 231.5 4.8 856 1 NCKX_DROME Q9u6a0 drosop 23 227 4.7 670 1 NKX2_RAT O54701 rattus 24 216.5 4.5 651 1 NKX2_CHICK Q9ial7 gallus 25 147 3.1 590 1 YKTA_CAEEL P34322 caenor 26 143.5 3.0 325 1 YRBG_ECOLI P45394 escher 26 143.5 3.0 325 1 YRBG_ECOLI P45394 escher 27 142.5 3.0 1807 1 ITB4_RAT Q64632 rattus 28 142 3.0 302 1 Y091_METJA Q57556 methan 29 141.5 2.9 572 1 YKT4_CAEEL P34315 caenor 30 128.5 2.7 664 1 SYM_BACSU P37465 bacill 31					_			
21 239.5 5.0 661 1 NKX2_HUMAN						_		
22 231.5 4.8 856 1 NCKX_DROME Q9u6a0 drosop 23 227 4.7 670 1 NKX2_RAT 054701 rattus 24 216.5 4.5 651 1 NKX2_CHICK Q9ial7 gallus 25 147 3.1 590 1 YKTA_CAEEL P34322 caenor 26 143.5 3.0 325 1 YRBG_ECOLI P45394 escher 27 142.5 3.0 1807 1 ITB4_RAT Q64632 rattus 28 142 3.0 302 1 Y091_METJA Q57556 methan 29 141.5 2.9 572 1 YKT4_CAEEL P34315 caenor 30 128.5 2.7 664 1 SYM_BACSU P37465 bacilli 31 128.5 2.7 4655 1 LRP2_HUMAN P98164 homo s 32 127 2.6 1822 1 ITB4_HUMAN P16144 homo s 33 125 2.6 700 1 TRDN_CANFA P82179 can 34					_			
23 227 4.7 670 1 NKX2_RAT 054701 rattus 24 216.5 4.5 651 1 NKX2_CHICK Q9ia17 gallus 25 147 3.1 590 1 YKTA_CAEEL P34322 caenor 26 143.5 3.0 325 1 YRBG_ECOLI P45394 escher 27 142.5 3.0 1807 1 ITB4_RAT Q64632 rattus 28 142 3.0 302 1 Y091_METJA Q57556 methan 29 141.5 2.9 572 1 YKT4_CAEEL P34315 caenor 30 128.5 2.7 664 1 SYM_BACSU P37465 bacill 31 128.5 2.7 4655 1 LRP2_HUMAN P98164 homo s 32 127 2.6 1822 1 ITB4_HUMAN P16144 homo s 33 125 2.6 700 1 TRDN_CANFA P82179 canis 34 120 2.5 1828 1 MAP2_MOUSE P20357 mus mus 35					_			_
24 216.5 4.5 651 1 NKX2_CHICK Q9ial7 gallus 25 147 3.1 590 1 YKTA_CAEEL P34322 caenor 26 143.5 3.0 325 1 YRBG_ECOLI P45394 escher 27 142.5 3.0 1807 1 ITB4_RAT Q64632 rattus 28 142 3.0 302 1 Y091_METJA Q57556 methand 29 141.5 2.9 572 1 YKT4_CAEEL P34315 caenor 30 128.5 2.7 664 1 SYM_BACSU P37465 bacill 31 128.5 2.7 4655 1 LRP2_HUMAN P98164 homo sc 32 127 2.6 1822 1 ITB4_HUMAN P16144 homo sc 33 125 2.6 700 1 TRDN_CANFA P82179 canis 34 120 2.5 1828 1 MAP2_MOUSE P20357 mus mus 35 119.5 2.5 673 1 SYM_CEIH P59079 oceanol 37 <td></td> <td></td> <td></td> <td></td> <td>1</td> <td>_</td> <td>Q9u6a0</td> <td>drosophila</td>					1	_	Q9u6a0	drosophila
25 147 3.1 590 1 YKTA_CAEEL P34322 caenors 26 143.5 3.0 325 1 YRBG_ECOLI P45394 escher. 27 142.5 3.0 1807 1 ITB4_RAT Q64632 rattus 28 142 3.0 302 1 Y091_METJA Q57556 methand 29 141.5 2.9 572 1 YKT4_CAEEL P34315 caenors 30 128.5 2.7 664 1 SYM_BACSU P37465 bacilly 31 128.5 2.7 4655 1 LRP2_HUMAN P98164 homo si 32 127 2.6 1822 1 ITB4_HUMAN P16144 homo si 33 125 2.6 700 1 TRDN_CANFA P82179 canis 34 120 2.5 1828 1 MAP2_MOUSE P20357 mus mus 35 119.5 2.5 1564 1 MRP2_RABIT Q28689 orycto 36 119 2.5 673 1 SYM_OCEIH P59079 oceanol 37 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister 38 118 2.5 803 1 RIR1_CRYPV O61065 cryptos 39 116.5 2.4 664 1 SYM_LISIN Q92f90 lister 40 116 2.4 657 1 SYM_STAAM Q99wb3 staphy 41 116 2.4 657 1 SYM_STAAM Q8ny00 staphy 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlich	23				1		054701	rattus norv
26 143.5 3.0 325 1 YRBG_ECOLI P45394 escher 27 142.5 3.0 1807 1 ITB4_RAT Q64632 rattus 28 142 3.0 302 1 Y091_METJA Q57556 methan 29 141.5 2.9 572 1 YKT4_CAEEL P34315 caenor 30 128.5 2.7 664 1 SYM_BACSU P37465 bacill 31 128.5 2.7 4655 1 LRP2_HUMAN P98164 homo scance 32 127 2.6 1822 1 ITB4_HUMAN P16144 homo scance 33 125 2.6 700 1 TRDN_CANFA P82179 canis 34 120 2.5 1828 1 MAP2_MOUSE P20357 mus mus 35 119.5 2.5 1564 1 MRP2_RABIT Q28689 orycto 36 119 2.5 673 1 SYM_DISMO Q8yaf2 lister 38 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister <td< td=""><td>24</td><td>216.5</td><td>4.5</td><td>651</td><td>1</td><td>NKX2_CHICK</td><td>Q9ial7</td><td>gallus gall</td></td<>	24	216.5	4.5	651	1	NKX2_CHICK	Q9ial7	gallus gall
27 142.5 3.0 1807 1 ITB4_RAT Q64632 rattus 28 142 3.0 302 1 Y091_METJA Q57556 methan 29 141.5 2.9 572 1 YKT4_CAEEL P34315 caenor 30 128.5 2.7 664 1 SYM_BACSU P37465 bacilla 31 128.5 2.7 4655 1 LRP2_HUMAN P98164 homo samula 32 127 2.6 1822 1 ITB4_HUMAN P16144 homo samula 33 125 2.6 700 1 TRDN_CANFA P82179 canis 34 120 2.5 1828 1 MAP2_MOUSE P20357 mus mus 35 119.5 2.5 1564 1 MRP2_RABIT Q28689 orycto 36 119 2.5 673 1 SYM_OCEIH P59079 oceanol 37 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister 39 116.5 2.4 664 1 SYM_STAAM Q99wb3 staphy <t< td=""><td>25</td><td>147</td><td>3.1</td><td>590</td><td>1</td><td>YKTA CAEEL</td><td>P34322</td><td>caenorhabdi</td></t<>	25	147	3.1	590	1	YKTA CAEEL	P34322	caenorhabdi
28 142 3.0 302 1 Y091_METJA Q57556 methand 29 141.5 2.9 572 1 YKT4_CAEEL P34315 caenord 30 128.5 2.7 664 1 SYM_BACSU P37465 bacille 31 128.5 2.7 4655 1 LRP2_HUMAN P98164 homo sa 32 127 2.6 1822 1 ITB4_HUMAN P16144 homo sa 33 125 2.6 700 1 TRDN_CANFA P82179 canis 34 120 2.5 1828 1 MAP2_MOUSE P20357 mus mus 35 119.5 2.5 1564 1 MRP2_RABIT Q28689 orycto 36 119 2.5 673 1 SYM_OCEIH P59079 oceanol 37 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister 38 118 2.5 803 1 RIRI_CRYPV O61065 cryptos 39 116.5 2.4 664 1 SYM_STAAM Q99wb3 staphy 40 </td <td>26</td> <td>143.5</td> <td>3.0</td> <td>325</td> <td>1</td> <td>YRBG ECOLI</td> <td>P45394</td> <td>escherichia</td>	26	143.5	3.0	325	1	YRBG ECOLI	P45394	escherichia
29 141.5 2.9 572 1 YKT4_CAEEL P34315 caenor 30 128.5 2.7 664 1 SYM_BACSU P37465 bacille 31 128.5 2.7 4655 1 LRP2_HUMAN P98164 homo sc 32 127 2.6 1822 1 ITB4_HUMAN P16144 homo sc 33 125 2.6 700 1 TRDN_CANFA P82179 canis 34 120 2.5 1828 1 MAP2_MOUSE P20357 mus mus 35 119.5 2.5 1564 1 MRP2_RABIT Q28689 orycto 36 119 2.5 673 1 SYM_OCEIH P59079 oceanol 37 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister 38 118 2.5 803 1 RIRI_CRYPV O61065 cryptos 39 116.5 2.4 664 1 SYM_LISIN Q92f90 lister 40 116 2.4 657 1 SYM_STAAW Q8ny00 staphy 41	27	142.5	3.0	1807	1	ITB4_RAT	Q64632	rattus norv
30 128.5 2.7 664 1 SYM_BACSU P37465 bacille 31 128.5 2.7 4655 1 LRP2_HUMAN P98164 homo se 32 127 2.6 1822 1 ITB4_HUMAN P16144 homo se 33 125 2.6 700 1 TRDN_CANFA P82179 canis 34 120 2.5 1828 1 MAP2_MOUSE P20357 mus mus 35 119.5 2.5 1564 1 MRP2_RABIT Q28689 orycto 36 119 2.5 673 1 SYM_OCEIH P59079 oceanol 37 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister 38 118 2.5 803 1 RIRI_CRYPV O61065 cryptos 39 116.5 2.4 664 1 SYM_STAAM Q99wb3 staphy 40 116 2.4 657 1 SYM_STAAW Q8ny00 staphy 41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy 42	28	142	3.0	302	1	Y091_METJA	Q57556	methanococc
31 128.5 2.7 4655 1 LRP2_HUMAN P98164 homo some services 32 127 2.6 1822 1 ITB4_HUMAN P16144 homo some services 33 125 2.6 700 1 TRDN_CANFA P82179 canis 34 120 2.5 1828 1 MAP2_MOUSE P20357 mus mus 35 119.5 2.5 1564 1 MRP2_RABIT Q28689 oryctom 36 119 2.5 673 1 SYM_OCEIH P59079 oceanol 37 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister 38 118 2.5 803 1 RIRI_CRYPV O61065 cryptom 39 116.5 2.4 664 1 SYM_LISIN Q92f90 lister 40 116 2.4 657 1 SYM_STAAM Q99wb3 staphy 41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus <tr< td=""><td>29</td><td>141.5</td><td>2.9</td><td>572</td><td>1</td><td>YKT4 CAEEL</td><td>P34315</td><td>caenorhabdi</td></tr<>	29	141.5	2.9	572	1	YKT4 CAEEL	P34315	caenorhabdi
32 127 2.6 1822 1 ITB4_HUMAN P16144 homo si 33 125 2.6 700 1 TRDN_CANFA P82179 canis 34 120 2.5 1828 1 MAP2_MOUSE P20357 mus mus 35 119.5 2.5 1564 1 MRP2_RABIT Q28689 orycto 36 119 2.5 673 1 SYM_OCEIH P59079 oceanol 37 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister 38 118 2.5 803 1 RIR1_CRYPV O61065 cryptos 39 116.5 2.4 664 1 SYM_LISIN Q92f90 lister 40 116 2.4 657 1 SYM_STAAM Q99wb3 staphy 41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlic	30	128.5	2.7	664	1	SYM_BACSU	P37465	bacillus su
33 125 2.6 700 1 TRDN_CANFA P82179 canis 34 120 2.5 1828 1 MAP2_MOUSE P20357 mus mus 35 119.5 2.5 1564 1 MRP2_RABIT Q28689 orycto 36 119 2.5 673 1 SYM_OCEIH P59079 oceanol 37 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister 38 118 2.5 803 1 RIR1_CRYPV O61065 cryptos 39 116.5 2.4 664 1 SYM_LISIN Q92f90 lister 40 116 2.4 657 1 SYM_STAAM Q99wb3 staphy 41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlich	31	128.5	2.7	4655	1	LRP2 HUMAN	P98164	homo sapien
34 120 2.5 1828 1 MAP2_MOUSE P20357 mus mus 35 119.5 2.5 1564 1 MRP2_RABIT Q28689 orycto 36 119 2.5 673 1 SYM_OCEIH P59079 oceano 37 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister 38 118 2.5 803 1 RIR1_CRYPV O61065 crypto 39 116.5 2.4 664 1 SYM_LISIN Q92f90 lister 40 116 2.4 657 1 SYM_STAAM Q99wb3 staphy 41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlich	32	127	2.6	1822	1	ITB4_HUMAN	P16144	homo sapien
35 119.5 2.5 1564 1 MRP2_RABIT Q28689 oryctol 36 119 2.5 673 1 SYM_OCEIH P59079 oceanol 37 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister 38 118 2.5 803 1 RIR1_CRYPV O61065 cryptol 39 116.5 2.4 664 1 SYM_LISIN Q92f90 lister 40 116 2.4 657 1 SYM_STAAM Q99wb3 staphy 41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlich	33	125	2.6	700	1	TRDN CANFA	P82179	canis famil
36 119 2.5 673 1 SYM_OCEIH P59079 oceanod 37 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister: 38 118 2.5 803 1 RIRI_CRYPV O61065 crypto: 39 116.5 2.4 664 1 SYM_LISIN Q92f90 lister: 40 116 2.4 657 1 SYM_STAAM Q99wb3 staphy: 41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy: 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlich	34	120	2.5	1828	1	MAP2 MOUSE	P20357	mus musculu
37 118.5 2.5 664 1 SYM_LISMO Q8yaf2 lister: 38 118 2.5 803 1 RIR1_CRYPV O61065 crypto: 39 116.5 2.4 664 1 SYM_LISIN Q92f90 lister: 40 116 2.4 657 1 SYM_STAAM Q99wb3 staphy: 41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy: 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlich	35	119.5	2.5	1564	1	MRP2 RABIT	Q28689	oryctolagus
38 118 2.5 803 1 RIRI_CRYPV 061065 cryptos 39 116.5 2.4 664 1 SYM_LISIN Q92f90 lister 40 116 2.4 657 1 SYM_STAAM Q99wb3 staphy 41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlich	36	119	2.5	673	1	SYM_OCEIH	P59079	oceanobacil
39 116.5 2.4 664 1 SYM_LISIN Q92f90 lister: 40 116 2.4 657 1 SYM_STAAM Q99wb3 staphy 41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlich	37	118.5	2.5	664	1	SYM_LISMO	Q8yaf2	listeria mo
39 116.5 2.4 664 1 SYM_LISIN Q92f90 lister: 40 116 2.4 657 1 SYM_STAAM Q99wb3 staphy: 41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy: 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlich	38	118	2.5	803	1	RIR1 CRYPV	061065	cryptospori
41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlich	39	116.5	2.4	664	1	SYM LISIN		
41 116 2.4 657 1 SYM_STAAW Q8ny00 staphy 42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlich	40	116	2.4	657	1	SYM STAAM	Q99wb3	staphylococ
42 115.5 2.4 1805 1 NEST_RAT P21263 rattus 43 115 2.4 548 1 CH60_EHRSE O32606 ehrlich	41	116	2.4	657	1	SYM STAAW		
-	42	115.5	2.4	1805	1	NEST_RAT		
44 114 2.4 1036 1 YAN2_SCHPO Q10068 schizos	43	115	2.4	548	1	CH60_EHRSE		
	44	114	2.4	1036	1	YAN2 SCHPO	Q10068	schizosacch
45 114 2.4 1468 1 RPOB_AQUAE 067762 aquife:	45	114	2.4	1468	1	RPOB_AQUAE		

ALIGNMENTS

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RESULT 1
NAC3 HUMAN
     NAC3 HUMAN
                     STANDARD;
                                     PRT;
                                             927 AA.
     P57103; Q8IUE9; Q8IUF0; Q8NFI7;
DT
     16-OCT-2001 (Rel. 40, Created)
     10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
DT
DT
DΕ
     Sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein
DE
     3).
GN
     SLC8A3 OR NCX3.
OS
     Homo sapiens (Human).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC
OX
     NCBI TaxID=9606;
RN
     [1]
RP
     SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).
RX
     MEDLINE=22294016; PubMed=12406570;
RA
     Gabellini N., Bortoluzzi S., Danieli G.A., Carafoli E.;
RT
     "The human SLC8A3 gene and the tissue-specific Na+/Ca2+ exchanger 3
RT
     isoforms.";
RL
     Gene 298:1-7(2002).
RN
RP
     SEQUENCE FROM N.A. (ISOFORM 3).
RX
     MEDLINE=22447378; PubMed=12558991;
```

```
Gabellini N., Bortoluzzi S., Danieli G.A., Carafoli E.;
RA
    "Control of the Na+/Ca2+ exchanger 3 promoter by cyclic adenosine
RT
RT
    monophosphate and Ca2+ in differentiating neurons.";
    J. Neurochem. 84:282-293(2003).
RL
RN
RP
    SEQUENCE OF 1-595 FROM N.A.
RA
    Kraev A.S., Chumakov I.M., Carafoli E.;
    "The organization of the human gene of the sodium-calcium exchanger.";
RT
RI.
    Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
    -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC
CC
        coupling. Ca(2+) is extruded from the cell during relaxation so as
CC
        to prevent overloading of intracellular stores (By similarity).
CC
    -!- ENZYME REGULATION: By intracellular calcium ions (By similarity).
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
    -!- ALTERNATIVE PRODUCTS:
CC
        Event=Alternative splicing; Named isoforms=3;
CC
        Name=3; Synonyms=NCX3.3;
CC
          IsoId=P57103-1; Sequence=Displayed;
CC
        Name=2; Synonyms=NCX3.2;
CC
          IsoId=P57103-2; Sequence=VSP 008116;
CC
        Name=4; Synonyms=NCX3.4;
CC
          IsoId=P57103-3; Sequence=VSP 008117, VSP 008118;
CC
    -!- TISSUE SPECIFICITY: Isoform 2 is expressed in brain and skeletal
CC
        muscle; Isoform 3 is expressed in excitable cells of brain, retina
        and skeletal muscle; Isoform 4 is expressed in skeletal muscle.
CC
CC
    CC
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    or send an email to license@isb-sib.ch).
CC
    ______
DR
    EMBL; AF510501; AAN60790.1; -.
DR
    EMBL; AF510502; AAN60791.1; -.
DR
    EMBL; AF510503; AAN60792.1; -.
DR
    EMBL; AF508982; AAM90955.1; -.
DR
    EMBL; X93017; -; NOT ANNOTATED CDS.
DR
    Genew; HGNC:11070; SLC8A3.
    MIM; 607991; -.
DR
    InterPro; IPR003644; Calx beta.
DR
DR
    InterPro; IPR004836; Na Ca Ex.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
    Pfam; PF03160; Calx-beta; 1.
DR
    Pfam; PF01699; Na Ca Ex; 2.
    PRINTS; PR01259; NACAEXCHNGR.
DR
DR
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KW
    Transport; Antiport; Calcium transport; Sodium transport;
KW
    Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW
    Calmodulin-binding; Repeat; Alternative splicing.
FT
    SIGNAL
                 1
                        30
                                POTENTIAL.
    CHAIN
                 31
                       927
FT
                                SODIUM/CALCIUM EXCHANGER 3.
FT
    DOMAIN
                 31
                       73
                                EXTRACELLULAR (POTENTIAL).
                74
FT
                       94
    TRANSMEM
                                POTENTIAL.
FT
    DOMAIN
                95
                       147
                                CYTOPLASMIC (POTENTIAL).
FT
    TRANSMEM
                148
                       168
                               POTENTIAL.
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169
                               EXTRACELLULAR (POTENTIAL).
FT
    DOMAIN
                      169
               170
FT
    TRANSMEM
                      190
                               POTENTIAL.
               191
FT
    DOMAIN
                      202
                               CYTOPLASMIC (POTENTIAL).
               203
FT
    TRANSMEM
                      223
                               POTENTIAL.
               224
FT
    DOMAIN
                      230
                               EXTRACELLULAR (POTENTIAL).
               231
FT
    TRANSMEM
                      251
                               POTENTIAL.
               252
FT
    DOMAIN
                      726
                               CYTOPLASMIC (POTENTIAL).
    TRANSMEM
               727
FT
                      747
                               POTENTIAL.
FT
    DOMAIN
               748
                      754
                               EXTRACELLULAR (POTENTIAL).
               755
FT
    TRANSMEM
                      775
                               POTENTIAL.
FT
    DOMAIN
               776
                      778
                               CYTOPLASMIC (POTENTIAL).
    TRANSMEM
FΤ
               779
                      799
                               POTENTIAL.
FT
               800
                      828
                               EXTRACELLULAR (POTENTIAL).
    DOMAIN
FT
    TRANSMEM
               829
                      849
                               POTENTIAL.
               850
FT
    DOMAIN
                      860
                               CYTOPLASMIC (POTENTIAL).
    TRANSMEM
               861
FT
                      881
                               POTENTIAL.
FT
    DOMAIN
               882
                      903
                               EXTRACELLULAR (POTENTIAL).
FT
    TRANSMEM
               904
                      924
                               POTENTIAL.
FT
    DOMAIN
               925
                      927
                               CYTOPLASMIC (POTENTIAL).
               253
FT
    DOMAIN
                      272
                               CALMODULIN-BINDING (BY SIMILARITY).
    REPEAT
               140
FT
                      180
                               ALPHA-1.
    REPEAT
               399
                               BETA-1.
FT
                      470
FT
    REPEAT
               534
                      604
                               BETA-2.
FT
    REPEAT
               796
                      832
                               ALPHA-2.
FT
    CARBOHYD
                45
                       45
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD
               823
                      823
FT
                               N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    VARSPLIC
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                      635
                               Missing (in isoform 2).
FT
                               /FTId=VSP 008116.
FT
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               596
                      620
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FT
                               GQEDSRDGKASIG (in isoform 4).
FT
                               /FTId=VSP 008117.
FT
    VARSPLIC
               621
                      927
                               Missing (in isoform 4).
FT
                               /FTId=VSP 008118.
SO
    SEOUENCE
              927 AA:
                      103009 MW;
                                  7B43CB6A9D77615E CRC64;
 Query Match
                        99.7%;
                               Score 4784; DB 1;
                                                 Length 927;
 Best Local Similarity
                        99.4%;
                               Pred. No. 1.5e-300;
 Matches 921; Conservative
                              0: Mismatches
                                              0;
                                                  Indels
                                                           6;
                                                               Gaps
                                                                      1;
Qу
           1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
             Db
           1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
Qy
          61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSOEREVTIKKPNGE 120
             Db
          61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Qy
         121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
             121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Db
Qy
         181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVOVWEGLLTLFF 240
             Db
         181 IIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
         241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qу
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Db	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qу	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Db	301	LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Qу	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Qу	421	KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Db	421	KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Qу	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qу	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Qy	601	KIVDEEEYERQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVL 654
Db	601	KIVDEEEYERQENFFIALGEPKWMERGISALLLSPDVTDRKLTMEEEEAKRIAEMGKPVL 660
Qу	655	GEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 714
Db	661	GEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG 720
Qу	715	EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFG 774
Db	721	EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFG 780
Qу	775	CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 834
Db	781	CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW 840
Qу	835	SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLA 894
Db	841	SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLA 900
Qу	895	TTWLFVSLWLLYILFATLEAYCYIKGF 921
Db	901	TTWLFVSLWLLYILFATLEAYCYIKGF 927
RESU: NAC3 ID AC DT DT DT DE	_RAT NAC3_RAT P70549; 01-NOV-19 01-NOV-19 28-FEB-20 Sodium/ca	STANDARD; PRT; 927 AA. 997 (Rel. 35, Created) 997 (Rel. 35, Last sequence update) 003 (Rel. 41, Last annotation update) alcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein
DE	3).	

GN

SLC8A3 OR NCX3.

```
os
    Rattus norvegicus (Rat).
oc
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC
OX
    NCBI TaxID=10116;
RN
    [1]
    SEQUENCE FROM N.A.
RP
RC
    STRAIN=Sprague-Dawley; TISSUE=Brain;
    MEDLINE=96394663; PubMed=8798769;
    Nicoll D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
RA
RA
    Philipson K.D.;
RT
    "Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.";
    J. Biol. Chem. 271:24914-24921(1996).
RL
CC
    -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC
        coupling. Ca(2+) is extruded from the cell during relaxation so as
CC
        to prevent overloading of intracellular stores.
CC
    -!- ENZYME REGULATION: By intracellular calcium ions.
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
    -!- TISSUE SPECIFICITY: Expression restricted to brain and skeletal
CC
        muscle.
    ______
CC
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    or send an email to license@isb-sib.ch).
    _____
CC
DR
    EMBL; U53420; AAC52817.1; -.
    InterPro; IPR003644; Calx beta.
    InterPro; IPR004836; Na Ca Ex.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
DR
    Pfam; PF03160; Calx-beta; 2.
DR
    Pfam; PF01699; Na Ca Ex; 2.
DR
    PRINTS; PR01259; NACAEXCHNGR.
DR
    SMART; SM00237; Calx beta; 2.
DR
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KW
    Transport; Antiport; Calcium transport; Sodium transport;
KW
    Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW
    Calmodulin-binding; Repeat.
FT
    SIGNAL
                1
                       30
                               POTENTIAL.
                      927
FT
    CHAIN
                31
                               SODIUM/CALCIUM EXCHANGER 3.
FT
               31
                      73
    DOMAIN
                               EXTRACELLULAR (POTENTIAL).
               74
                      94
\mathbf{FT}
    TRANSMEM
                               POTENTIAL.
               95
                      147
FT
    DOMAIN
                               CYTOPLASMIC (POTENTIAL).
    TRANSMEM
               148
                      168
FT
                               POTENTIAL.
FT
    DOMAIN
               169
                      169
                               EXTRACELLULAR (POTENTIAL).
FT
    TRANSMEM
               170
                      190
                               POTENTIAL.
FT
    DOMAIN
               191
                      202
                               CYTOPLASMIC (POTENTIAL).
FT
    TRANSMEM
               203
                      223
                               POTENTIAL.
FT
    DOMAIN
               224
                      230
                               EXTRACELLULAR (POTENTIAL).
FT
    TRANSMEM
               231
                      251
                               POTENTIAL.
                               CYTOPLASMIC (POTENTIAL).
FT
    DOMAIN
               252
                      726
FT
               727
                      747
    TRANSMEM
                               POTENTIAL.
FT
    DOMAIN
               748
                      754
                               EXTRACELLULAR (POTENTIAL).
FT
                      775
    TRANSMEM
               755
                               POTENTIAL.
                      778
FT
               776
    DOMAIN
                               CYTOPLASMIC (POTENTIAL).
```

```
800
FT
    DOMAIN
                   828
                           EXTRACELLULAR (POTENTIAL).
             829
    TRANSMEM
                   849
FT
                           POTENTIAL.
    DOMAIN
             850
                   860
                           CYTOPLASMIC (POTENTIAL).
FT
FT
    TRANSMEM
             861
                   881
                           POTENTIAL.
             882
                   903
    DOMAIN
                           EXTRACELLULAR (POTENTIAL).
FT
             904
FT
    TRANSMEM
                   924
                           POTENTIAL.
             925
                   927
FT
    DOMAIN
                           CYTOPLASMIC (POTENTIAL).
             253
                   272
                           CALMODULIN-BINDING (BY SIMILARITY).
FT
    DOMAIN
FT
    REPEAT
             140
                   180
                           ALPHA-1.
FT
    REPEAT
             399
                   470
                           BETA-1.
FT
    REPEAT
             534
                   604
                           BETA-2.
             796
                   832
                           ALPHA-2.
    REPEAT
FΤ
    DOMAIN
             645
                   648
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FT
                           N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
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              45
                    45
                           N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
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    SEQUENCE
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SQ
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                           Score 4686; DB 1; Length 927;
 Query Match
                           Pred. No. 3.1e-294;
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 Best Local Similarity
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 Matches 897; Conservative
                          14;
                                         10;
                                            Indels
                                                     6;
                                                        Gaps
                                                               1;
         1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
Qу
           1 MAWLRLOPLTSAFLHFGLVTFVLFLNGLRAEAGDLRDVPSAGQNNESCSGSSDCKEGVIL 60
Db
         61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Qу
           61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Db
        121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Qy
           121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Db
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Qу
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Db
        241 FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qу
           241 FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIIETEGEHPKGIEMDGKMMNSHFLDGN 300
Db
        301 LVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Qу
           301 LIPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Db
        361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Qу
           361 MMTGAGNILKKHAAEOAKKTASMSEVHTDEPEDFASKVFFDPCSYOCLENCGAVLLTVVR 420
Db
        421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
Qу
           421 KGGDISKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETOKEFSVGIIDDDIFEEDEHF 480
Db
        481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qy
           481 FVRLSNVRVEEEQLEEGMTPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Db
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POTENTIAL.

779

799

TRANSMEM

FT

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541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRV 600
Qу
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QУ
            Db
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Qу
            Dh
        661 GEHPKLEVIIEESYEFKSTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEEEDESG 720
        715 EERLPSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFG 774
Qy _
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Db
Qу
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            Db
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Qу
        835 SVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLA 894
            Db
        841 SVAAIYWAMOGOEFHVSAGTLAFSVTLFTIFAFVCLSVLLYRRRPHLGGELGGPRGCKLA 900
Qу
        895 TTWLFVSLWLLYILFATLEAYCYIKGF 921
            11111111111111111111111111111
Db
        901 TTWLFVSLWLLYVLFATLEAYCYIKGF 927
RESULT 3
NAC1 CANFA
    NAC1 CANFA
                 STANDARD;
                             PRT:
                                   970 AA.
    P23685;
AC
DT
    01-NOV-1991 (Rel. 20, Created)
DT
    01-NOV-1991 (Rel. 20, Last sequence update)
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
DΕ
    1).
GN
    SLC8A1.
os
    Canis familiaris (Dog).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX
    NCBI TaxID=9615;
RN
    [1]
    SEQUENCE FROM N.A.
RP
RC
    TISSUE=Heart;
RX
    MEDLINE=91047958; PubMed=1700476;
RA
    Nicoll D.A., Longoni S., Philipson K.D.;
RT
    "Molecular cloning and functional expression of the cardiac
RT
    sarcolemmal Na(+)-Ca2+ exchanger.";
RL
    Science 250:562-565(1990).
RN
    [2]
    SEQUENCE FROM N.A.
RP
RC
    TISSUE=Heart;
RX
    MEDLINE=92152737; PubMed=1785844;
RA
    Nicoll D.A., Philipson K.D.;
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RT
    "Molecular studies of the cardiac sarcolemmal sodium-calcium
    exchanger.";
RT
    Ann. N.Y. Acad. Sci. 639:181-188(1991).
RL
CC
    -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC
        coupling. Ca(2+) is extruded from the cell during relaxation so as
CC
        to prevent overloading of intracellular stores.
    -!- ENZYME REGULATION: By ATP.
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC
CC
    -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
CC
    -----
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    entities requires a license agreement (See http://www.isb-sib.ch/announce/
    or send an email to license@isb-sib.ch).
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KW
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FT
              756
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    MOD RES
              389
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                    389
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                         1 :11 :: : 11
           1 111 1 1
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Db
        628 -----ISDVTDRK--LTMEEEEAKRIAEMGKPVLGEHPKLEVI 663
Qy
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        653 YGQPVFRKVHAREHPIPSTVITIAEEYDDKQPLTSKEEEERRIAEMGRPILGEHTKLEVI 712
Qv
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Db
        724 YVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSV 783
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        844 QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLW 903
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             Db
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    01-FEB-1996 (Rel. 33, Created)
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    28-FEB-2003 (Rel. 41, Last annotation update)
DE
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DE
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GN
    SLC8A1 OR NCX1.
os
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OC
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    TISSUE=Heart;
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    Menick D.R., Barnes K.V., Thacker U.F., Dawson M.M.,
RA
    McDermott D.E., Rozich J.D., Kent R.L., Cooper G.;
RT
    "The exchanger and cardiac hypertrophy.";
RL
    Ann. N.Y. Acad. Sci. 779:489-501(1996).
RN
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RP
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RX
    MEDLINE=97269065; PubMed=9111065;
RA
    Barnes K.V., Cheng G., Dawson M.M., Menick D.R.;
RT
    "Cloning of cardiac, kidney, and brain promoters of the feline ncxl
RT
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J. Biol. Chem. 272:11510-11517(1997).
RL
    -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction .
CC
        coupling. Ca(2+) is extruded from the cell during relaxation so as
CC
        to prevent overloading of intracellular stores.
CC
    -!- ENZYME REGULATION: By ATP.
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC
    -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
CC
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    or send an email to license@isb-sib.ch).
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    Pfam; PF03160; Calx-beta; 2.
    Pfam; PF01699; Na Ca Ex; 2.
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    PRINTS; PR01259; NACAEXCHNGR.
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    SMART; SM00237; Calx beta; 2.
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KW
    Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW
    Calmodulin-binding; Repeat.
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FT
    REPEAT
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539
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              689
    DOMAIN
                   692
                           POLY-GLU.
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Db
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Qу
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Db
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DT
    16-OCT-2001 (Rel. 40, Last sequence update)
DT
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    10-OCT-2003 (Rel. 42, Last annotation update)
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GN
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    Komuro I., Wenninger K.E., Philipson K.D., Izumo S.;
RA
RT
    "Molecular cloning and characterization of the human cardiac Na+/Ca2+
RT
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    Proc. Natl. Acad. Sci. U.S.A. 89:4769-4773(1992).
RL
RN
    SEQUENCE FROM N.A. (ISOFORMS 3 AND 7).
RP
RX
    MEDLINE=21136211; PubMed=11241183;
RA
    Van Eylen F., Bollen A., Herchuelz A.;
RT
    "NCX1 Na/Ca exchanger splice variants in pancreatic islet cells.";
RL
    J. Endocrinol. 168:517-526(2001).
RN
    [3]
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RP
     SEQUENCE FROM N.A. (ISOFORM 7).
RA.
     Mangini N.J., Chen W., Wang Q., Kennedy B.G.;
RT
     "Na+/Ca2+ exchanger isoforms in cultured human retinal pigment
RT
     epithelium.";
     Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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RN
RP
     SEQUENCE OF 1-603 FROM N.A.
RA
     Rohlfing T., Strowmatt C., Scronce D., Moody T.;
RL
     Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN
RP
     SEQUENCE OF 850-973 FROM N.A.
     Kozlowicz A., Stoneking T., Hawkins M., Le T.;
RA
RL
     Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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RP
     SEQUENCE OF 459-681 FROM N.A. (ISOFORM 10).
     Lundquist P., Lundgren T., Gritli-Linde A., Linde A.;
RA
     Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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CC
     -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC
         coupling. Ca(2+) is extruded from the cell during relaxation so as
CC
         to prevent overloading of intracellular stores.
CC
     -!- ENZYME REGULATION: By ATP.
CC
     -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC
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CC
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           IsoId=P32418-4; Sequence=VSP 003397, VSP 003398;
CC
     -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
CC
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     between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
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DR
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DR
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     GO; GO:0015085; F:calcium ion transporter activity; TAS.
DR
     GO; GO:0015081; F:sodium ion transporter activity; TAS.
DR
     GO; GO:0006816; P:calcium ion transport; TAS.
DR
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DR
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DR
     GO; GO:0006814; P:sodium ion transport; TAS.
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DR
     InterPro; IPR004837; NaCa Exmemb.
DR
     Pfam; PF03160; Calx-beta; 2.
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 Query Match
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 Best Local Similarity
                    68.9%; Pred. No. 7.7e-214;
 Matches 674; Conservative 111; Mismatches 128; Indels
                                                  65; Gaps
                                                            10;
Qу
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                     | | : | | :: : | |
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                                            ||:
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        408 LENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETOKEFSVG 467
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        468 IIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
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            Db
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Db
RESULT 6
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DT
    01-FEB-1996 (Rel. 33, Created)
    01-FEB-1996 (Rel. 33, Last sequence update)
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
DE
    Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
DE
    1).
GN
    SLC8A1.
os
    Cavia porcellus (Guinea pig).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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RP
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RC
    TISSUE=Heart;
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    Tsuruya Y., Bersohn M.M., Li Z., Nicoll D.A., Philipson K.D.;
RA
RT
    "Molecular cloning and functional expression of the guinea pig
    cardiac Na(+)-Ca2+ exchanger.";
RT
RL
    Biochim. Biophys. Acta 1196:97-99(1994).
CC
    -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
        coupling. Ca(2+) is extruded from the cell during relaxation so as
CC
        to prevent overloading of intracellular stores.
CC
    -!- ENZYME REGULATION: By ATP.
CC
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
    -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
CC
CC
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CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
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CC
     entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
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DR
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DR
DR
    Pfam; PF03160; Calx-beta; 2.
    Pfam; PF01699; Na Ca Ex; 2.
DR
DR
    PRINTS; PR01259; NACAEXCHNGR.
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DR
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    DOMAIN
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Qy	664	<pre>IEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFD </pre>	723
Db	713	3 IEESYEFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKLPSCFD	
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Db
         773 YVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSV 832
         784 TAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWAL 843
Qу
             833 TAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAA 892
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         844 QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLW 903
Qу
              Db
         893 NGEQFKVSPGTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSCLFVLLW 952
Qy
         904 LLYILFATLEAYCYIKGF 921
             1111 1::1111:111
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         953 LLYIFFSSLEAYCHIKGF 970
RESULT 7
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AC
    001728;
    01-JUL-1993 (Rel. 26, Created)
DT
DT
    01-JUN-1994 (Rel. 29, Last sequence update)
DT
    10-OCT-2003 (Rel. 42, Last annotation update)
    Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
DΕ
    1).
    SLC8A1 OR NCX1.
GN
OS
    Rattus norvegicus (Rat).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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    NCBI TaxID=10116;
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    [1]
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    TISSUE=Heart;
RX
    MEDLINE=93138118; PubMed=8422940;
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    Low W., Kasir J., Rahamimoff H.;
    "Cloning of the rat heart Na(+)-Ca2+ exchanger and its functional
RT
RT
    expression in HeLa cells.";
RL
    FEBS Lett. 316:63-67(1993).
RN
RP
    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC
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RX
    MEDLINE=93202244; PubMed=8454039;
    Furman I., Cook O., Kasir J., Rahamimoff H.;
RA
RT
    "Cloning of two isoforms of the rat brain Na(+)-Ca2+ exchanger gene
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    and their functional expression in HeLa cells.";
RL
    FEBS Lett. 319:105-109(1993).
RN
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RP
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RC
    STRAIN=Sprague-Dawley; TISSUE=Kidney cortex;
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RA
    Lee S.-L., Yu A.S.L., Lytton J.;
    "Tissue-specific expression of Na(+)-Ca2+ exchanger isoforms.";
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RL
    J. Biol. Chem. 269:14849-14852(1994).
RN
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    TISSUE SPECIFICITY.
RP
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RX
    MEDLINE=96394663; PubMed=8798769;
    Nicoll D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
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RA
     Philipson K.D.;
RT
     "Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.";
RL
     J. Biol. Chem. 271:24914-24921(1996).
     -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC
CC
         coupling. Ca(2+) is extruded from the cell during relaxation so as
CC
         to prevent overloading of intracellular stores.
     -!- ENZYME REGULATION: By ATP.
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC
CC
     -!- ALTERNATIVE PRODUCTS:
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CC
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          IsoId=Q01728-2; Sequence=VSP 003402, VSP_003403;
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CC
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CC
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CC
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CC
        Name=5; Synonyms=Kidney-2, NaCa3;
          IsoId=Q01728-5; Sequence=VSP 003401, VSP 003402, VSP 003404;
CC
CC
    -!- TISSUE SPECIFICITY: Cardiac sarcolemma or brain, and spleen.
CC
    CC
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CC
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    the European Bioinformatics Institute. There are no restrictions on its
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    use by non-profit institutions as long as its content is in no way
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    modified and this statement is not removed. Usage by and for commercial
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    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
CC
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DR
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DR
    EMBL; X68812; CAA48707.1; -.
DR
    EMBL; X68813; CAA48708.1; -.
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DR
    EMBL; U04934; AAA19124.1; -.
DR
    EMBL; U04936; AAA19125.1; -.
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    PIR; A53789; A53789.
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    PIR; S32435; S32435.
    PIR; S43730; S43730.
DR
DR
    InterPro; IPR003644; Calx beta.
DR
    InterPro; IPR004836; Na Ca Ex.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
    Pfam; PF03160; Calx-beta; 2.
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    Pfam; PF01699; Na Ca Ex; 2.
    PRINTS; PR01259; NACAEXCHNGR.
DR
    SMART; SM00237; Calx beta; 2.
DR
DR
    TIGRFAMs; TIGR00845; caca; 1.
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    Transport; Antiport; Calcium transport; Sodium transport;
KW
    Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW
    Calmodulin-binding; Repeat; Alternative splicing.
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\mathbf{FT}
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FT
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\mathbf{FT}
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FT
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                        635
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                                  4 and isoform 5).
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                                  Missing (\overline{in} \text{ isoform 2 and isoform 4}).
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                                  /FTId=VSP 003403.
FT
    VARSPLIC
                 649
                        677
                                  Missing (in isoform 3 and isoform 5).
FΤ
                                  /FTId=VSP 003404.
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                        250
                                  D \rightarrow A (IN REF. 1).
FT
                402
                        402
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                                  P \rightarrow A (IN REF. 1).
SQ
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                971 AA; 108184 MW; EC456CFE3AFC6A69 CRC64;
                          71.5%; Score 3428; DB 1; Length 971;
 Query Match
 Best Local Similarity 68.7%; Pred. No. 4.2e-213;
 Matches 675; Conservative 106; Mismatches 124; Indels 78; Gaps
                                                                            11:
            4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK 55
Qу
                    : : | | | | | |
                                                11 11:
                                                                  1:11
Db
            2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53
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           56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
              54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK 113
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Qу	293	NSHFLDGNLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS	345
Db	294	NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qу	346	HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT	412
Qу	405	YQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
Db	413	YQCLENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qу	465	SVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
Db	473	RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDGILDSNHVSAIACLGSPNTATITI	528
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Db	529	FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT	588
QУ	584	YGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMER	626
Db	589	CGELEFQNDEIVKTISVKVIDDEEYEKNKTFFIEIGEPRLVEMSEKKALLLNELGGFTLT	648
Qу	627	GISDVTDRKLTMEEEEAKRIAEMGKPVLGEHP	658
Db	649	EGKKMYGQPVFRKVHARDHPIPSTVISISEEYDDKQPLTSKEEEERRIAEMGRPILGEHT	708
Qу	659	KLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERL	718
Db	709	KLEVIIEESYEFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKL	768
Qу	719	PSCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIG	778
Db	769	PSCFDYVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIG	828
Qу	779	LKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAA	838
Db	829	LKDSVTAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAA	888
Qу	839	IYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWL	898
Dh	ឧឧឧ	::	9/8

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Qу
             Db
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RESULT 8
NAC1 BOVIN
   NAC1 BOVIN
                   STANDARD;
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                                         970 AA.
AC
     P48765;
     01-FEB-1996 (Rel. 33, Created)
DT
    01-FEB-1996 (Rel. 33, Last sequence update)
DT
     28-FEB-2003 (Rel. 41, Last annotation update)
     Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
DE
DE
    1).
GN
    SLC8A1.
os
    Bos taurus (Bovine).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
     Bovidae; Bovinae; Bos.
OX
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RC
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RA
    Aceto J.F., Condrescu M., Kroupis C., Nelson H., Nelson N.,
RA
    Nicoll D.A., Philipson K.D., Reeves J.P.;
RT
     "Cloning and expression of the bovine cardiac sodium-calcium
RT
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RL
    Arch. Biochem. Biophys. 298:553-560(1992).
RN
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RC
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    MEDLINE=90241959; PubMed=2334719;
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RA
RT
     "Identification of the sodium-calcium exchanger as the major
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    ricin-binding glycoprotein of bovine rod outer segments and its
RT
    localization to the plasma membrane.";
RL
    Biochemistry 29:1601-1607(1990).
CC
     -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC
        coupling. Ca(2+) is extruded from the cell during relaxation so as
CC
        to prevent overloading of intracellular stores.
CC
    -!- ENZYME REGULATION: By ATP.
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC
    -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
CC
    ______
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    the European Bioinformatics Institute. There are no restrictions on its
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    or send an email to license@isb-sib.ch).
CC
DR
    EMBL; L06438; AAA30509.1; -.
DR
    PIR; S27114; S27114.
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DR

InterPro; IPR003644; Calx_beta.
InterPro; IPR004836; Na Ca Ex.

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Pfam; PF03160; Calx-beta; 2.
DR
     Pfam; PF01699; Na Ca Ex; 2.
DR
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DR
     SMART; SM00237; Calx beta; 2.
     TIGRFAMs; TIGR00845; caca; 1.
DR
KW
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KW
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KW
     Calmodulin-binding; Repeat.
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                  72
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FT
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FT
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                 200
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                 872
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FT
     DOMAIN
                 893
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FT
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                        924
                                  POTENTIAL.
FΤ
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FT
                        270
     DOMAIN
                 251
                                  CALMODULIN-BINDING (POTENTIAL).
FT
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                 138
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FT
                 407
                        478
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     REPEAT
FT
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                 539
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FT
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     REPEAT
                 839
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FT
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                 236
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FT
                 689
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                                   POLY-GLU.
FT
     DOMAIN
                 756
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                                   POLY-ASP.
FT
                 389
                        389
                                   PHOSPHORYLATION (POTENTIAL).
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FT
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                  41
                        41
                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
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 Matches 672; Conservative 110; Mismatches 131;
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                                                                1:11
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           59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN 118
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DR

InterPro; IPR004837; NaCa Exmemb.

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Db	177	: :	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSH	295
Db .	237	: : : : :	296
Qy	296	FLDGNLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ	348
Db	297	VDSFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355
Qy	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC	407
Db	356	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTYQC	415
·Qy	408	LENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
Db	416	LENCGTVALTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG	475
Qу	468	<pre>IIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD </pre>	527
Db	476	IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVSTLACLGSPSTATVTIFDDD	532
Qу	528	HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL	587
Db	533	HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL	592
Qy	588	EFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERG	627
Db	593	EFQNDEIVKTISVKVIDDEEYEKNKTFFLEIGEPRLVEMSEKKALLLNELGGFTITGKYL	652
Qy	628	ISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVI	663
Db	653	YGQPVFRKVHAREHPLPSTIITIADEYDDKQPLTSKEEEERRIAEMGRPILGEHTRLEVI	712
Qy	664	<pre>IEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFD </pre>	723
Db	713	IEESYEFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKLPSCFD	772
QУ	724	YVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSV	783
Db	773	YVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFACTIALKDSV	832
Qу	784	TAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWAL	843
Db	833	TAVVFVALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAA	892
Qy	844	QGQEFHVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLW ::	903

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893 NGEQFKVSPGTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSCLFVLLW 952
Db
         904 LLYILFATLEAYCYIKGF 921
Qy
              1111 1::1111:111
Db
         953 LLYIFFSSLEAYCHIKGF 970
RESULT 9
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ID
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                   STANDARD; PRT; 970 AA.
    P70414;
AC
DT
    01-NOV-1997 (Rel. 35, Created)
DT
    01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
    Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
DE
DE
    1).
    SLC8A1 OR NCX.
GN
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
    SEQUENCE FROM N.A.
RP
RC
    STRAIN=C57BL/6;
RX
    MEDLINE=96250070; PubMed=8659820;
RA
    Kim I., Lee C.O.;
RT
    "Cloning of the mouse cardiac Na(+)-Ca2+ exchanger and functional
RT
    expression in Xenopus oocytes.";
RL
    Ann. N.Y. Acad. Sci. 779:126-128(1996).
CC
    -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC
        coupling. Ca(2+) is extruded from the cell during relaxation so as
CC
         to prevent overloading of intracellular stores.
CC
    -!- ENZYME REGULATION: By ATP.
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
    -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
CC
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    the European Bioinformatics Institute. There are no restrictions on its
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    or send an email to license@isb-sib.ch).
CC
DR
    EMBL; U70033; AAB46708.1; -.
    MGD; MGI:107956; Slc8a1.
DR
DR
    InterPro; IPR003644; Calx beta.
DR
    InterPro; IPRO04836; Na Ca Ex.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
    Pfam; PF03160; Calx-beta; 2.
DR
    Pfam; PF01699; Na Ca Ex; 2.
DR
    PRINTS; PR01259; NACAEXCHNGR.
DR
    SMART; SM00237; Calx beta; 2.
DR
    TIGRFAMs; TIGR00845; caca; 1.
KW
    Transport; Antiport; Calcium transport; Sodium transport;
KW
    Transmembrane; Glycoprotein; Phosphorylation; Signal;
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KW

Calmodulin-binding; Repeat.

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FT
     SIGNAL
                  1
                        32
                                 POTENTIAL.
     CHAIN
                 33
                       970
                                 SODIUM/CALCIUM EXCHANGER 1.
FΤ
FT
     DOMAIN
                 33
                        71
                                 EXTRACELLULAR (POTENTIAL).
                 72
FT
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                        93
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FT
     DOMAIN
                 94
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FT
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                134
                       155
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FT
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                156
                       167
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FT
    TRANSMEM
                168
                       188
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     DOMAIN
                189
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                       222
                                 POTENTIAL.
FT
     DOMAIN
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                226
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                                 POTENTIAL.
FΤ
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                250
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                797
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                                 POTENTIAL.
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                                 CYTOPLASMIC (POTENTIAL).
FT
    TRANSMEM
                822
                       840
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FT
                841
    DOMAIN
                       871
                                 EXTRACELLULAR (POTENTIAL).
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    TRANSMEM
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                                 POTENTIAL.
FT
    DOMAIN
                893
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FT
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                       924
                                 POTENTIAL.
FT
                925
    DOMAIN
                       941
                                 EXTRACELLULAR (POTENTIAL).
FT
                942
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FT
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                                 CYTOPLASMIC (POTENTIAL).
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FT
    DOMAIN
                251
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FT
    REPEAT
                138
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    REPEAT
FT
                407
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                                 BETA-1.
FT
    REPEAT
                539
                       609
                                 BETA-2.
FT
    REPEAT
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                                 ALPHA-2.
FT
    DOMAIN
                236
                       239
                                 POLY-PHE.
FT
    DOMAIN
                689
                       692
                                 POLY-GLU.
FT
    DOMAIN
                756
                       760
                                 POLY-ASP.
FT
    MOD RES
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                                 PHOSPHORYLATION (POTENTIAL).
FT
    CARBOHYD
                 41
                        41
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
FΤ
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                                Pred. No. 1.2e-211;
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                                                     Indels
                                                              59; Gaps
                                                                          8;
           4 LRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIW 63
Qу
                    : : | || | |
                                             : : |
                                                        1:11
                                                             Db
           2 LRLSLPPNVSMGFRLVALVALLFSHVDHITADTEAETGGNETTECTGSYYCKKGVILPIW 61
          64 YPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETST 123
Qу
              Db
          62 EPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPNGETTK 121
Qy
         124 TTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIG 183
             Db
         122 TTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIIA 181
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Qy
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Db 182 LCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTFFFFPI 241 244 CVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH---FL 297 Qу 242 CVVFAWVADRRLLFYKYVYKRYRAGKORGMIIEHEGDRPASKTEIEMDGKVVNSHVDNFL 301 Db 298 DGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHOOKSRAF 353 Qy 302 DGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQKSRAF 360 Db 354 YRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLENCG 412 Qу 361 YRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMEMAENDPVSKIFFEQGTYQCLENCG 420 Db 413 AVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDD 472 Qу 421 TVALTIMRRGGDLSTTVFVDFRTEDGTANAASDYEFTEGTVIFKPGETOKEIRVGIIDDD 480 Db 473 IFEEDEHFFVRLSNVRIEEEOPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIF 532 Qу 11||||:|| | |||||: : |:|: : :: 481 IFEEDENFLVHLSNVRVSSDVSEDGI---LESNHASSIACLGSPSTATITIFDDDHAGIF 537 Db 533 TFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKND 592 Qу Db 538 TFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDTCGEPEFOND 597 593 ETVKTIRVKIVDEEEYEROENFFIALGEPKWMERG----- 627 Qу Db 598 EIVKTISVKVIDDEEYEKNKTFFIEIGEPRLVEMSEKKALLLNELGGFTLTGKEMYGOPI 657 QУ -ISDVTDRK--LTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESY 668 11: 1 1 658 FRKVHARDHPIPSTVITISEEYDDKQPLTSKEEEERRIAEMGRPILGEHTKLEVIIQESY 717 Db 669 EFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHF 728 Qу 718 EFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKLPSCFDYVMHF 777 Db 729 LTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVF 788 Qу 778 LTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCTIGLKDSVTAVVF 837 Db 789 VAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEF 848 Qу 838 VALGTSVPDTFASKVAATQDQYADASIGNVTGSNAVNVFLGIGVAWSIAAIYHAANGEOF 897 Db 849 HVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYIL 908 Qу 898 KVSPGTLAFSVTLFTIFAFINVGVLLYRRRPEIGGELGGPRTAKLLTSSLFVLLWLLYIF 957 Db Qу 909 FATLEAYCYIKGF 921 1::11111:111

958 FSSLEAYCHIKGF 970

Db

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NAC2 HUMAN
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ID
AC
    Q9UPR5;
DT
    16-OCT-2001 (Rel. 40, Created)
    16-OCT-2001 (Rel. 40, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
    Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein
DE
DE
GN
    SLC8A2 OR NCX2 OR KIAA1087.
os
    Homo sapiens (Human).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX
    NCBI TaxID=9606;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=Brain;
RX
    MEDLINE=99397452; PubMed=10470851;
RA
    Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N.,
    Tanaka A., Kotani H., Nomura N., Ohara O.;
RA
RT
    "Prediction of the coding sequences of unidentified human genes. XIV.
RT
    The complete sequences of 100 new cDNA clones from brain which code
RT
    for large proteins in vitro.";
RL
    DNA Res. 6:197-205(1999).
CC
    -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC
        coupling. Ca(2+) is extruded from the cell during relaxation so as
CC
        to prevent overloading of intracellular stores (By similarity).
CC
    -!- ENZYME REGULATION: By ATP (By similarity).
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
    ______
CC
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    the European Bioinformatics Institute. There are no restrictions on its
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    or send an email to license@isb-sib.ch).
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    EMBL; AB029010; BAA83039.1; ALT INIT.
DR
    Genew; HGNC:11069; SLC8A2.
DR
    MIM; 601901; -.
DR
    InterPro; IPR003644; Calx beta.
    InterPro; IPR004836; Na_Ca_Ex.
DR
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    InterPro; IPR004837; NaCa Exmemb.
    Pfam; PF03160; Calx-beta; 2.
DR
DR
    Pfam; PF01699; Na Ca Ex; 2.
DR
    PRINTS; PR01259; NACAEXCHNGR.
    SMART; SM00237; Calx beta; 2.
DR
    TIGRFAMs; TIGR00845; caca; 1.
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KW
KW
    Transmembrane; Glycoprotein; Phosphorylation; Signal;
    Calmodulin-binding; Repeat.
KW
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FT
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                       90
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                91
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FT
                       130
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    TRANSMEM
                131
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FT
    DOMAIN
                153
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               223
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    TRANSMEM
               721
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FT
                              POTENTIAL.
               741
                     747
    DOMAIN
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                              EXTRACELLULAR (POTENTIAL).
    TRANSMEM
               748
                     770
FT
                              POTENTIAL.
                              CYTOPLASMIC (POTENTIAL).
FT
    DOMAIN
               771
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FT
    TRANSMEM
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FT
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                              POTENTIAL.
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               876
                     892
FT
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FT
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               910
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FT
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FT
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FT
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               135
                     175
                              ALPHA-1.
               397
                     468
                              BETA-1.
FT
    REPEAT
FT
    REPEAT
               527
                     597
                              BETA-2.
FT
    REPEAT
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                              ALPHA-2.
FT
    DOMAIN
                29
                      32
                              POLY-PRO.
FT
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FT
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FT
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 Best Local Similarity 71.0%; Pred. No. 1.3e-209;
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                                                              Gaps
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                    \mathbf{H}
Db
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         100 ASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHG 159
Qy
            95 AAIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHN 154
Db
         160 FIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYM 219
Qy
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Db
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Qу
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Db
         280 DHPKGIEMDGKMMNSHFLDGNL----VPLEGKEVDESRREMIRILKDLKQKHPEKDLDQ 334
Qу
            1 1
                                      275 DPPKSIELDGTFVGAE-APGELGGLGPGPAEARELDASRREVIQILKDLKQKHPDKDLEQ 333
Db
         335 LVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDF 394
Qу
            Db
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395 ISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVV 454
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        455 LKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEQ----PEEGMPPAIFNSLPLPR 510
Qу
            453 FKPGETQKELRIGIIDDDIFEEDEHFFVRLLNLRVGDAQGMFEPDGG-----GRPK 503
Db
        511 AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVE 570
Qу
                                 :|||| :| ::|:|:|:|||| :|:|||
             504 GRLVAPLLATVTILDDDHAGIFSFQDRLLHVSECMGTVDVRVVRSSGARGTVRLPYRTVD 563
Db
Qу
        571 GTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERGISD 630
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        564 GTARGGGVHYEDACGELEFGDDETMKTLQVKIVDDEEYEKKDNFFIELGQPQWLKRGISA 623
        631 VT-----DRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLA 684
Qу
                  Db
        624 LLLNQGDGDRKLTAEEEEARRIAEMGKPVLGENCRLEVIIEESYDFKNTVDKLIKKTNLA 683
        685 LVVGTHSWRDQFMEAITVSAAGDEDEDESG--EERLPSCFDYVMHFLTVFWKVLFACVPP 742
Qу
           684 LVIGTHSWREQFLEAITVS-AGDEEEEEDGSREERLPSCFDYVMHFLTVFWKVLFACVPP 742
Db
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Qу
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Db
        803 AAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLF 862
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Db
Qу
        863 TIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYILFATLEAYCYIKGF 921
           Db
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AC
    P48768;
    01-FEB-1996 (Rel. 33, Created)
DT
    01-FEB-1996 (Rel. 33, Last sequence update)
DT
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
    Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein
DE
DE
    2).
GN
    SLC8A2 OR NCX2.
OS
    Rattus norvegicus (Rat).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC
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OX
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RC
    STRAIN=Sprague-Dawley; TISSUE=Brain stem;
RX
   MEDLINE=94292496; PubMed=8021246;
    Li Z., Matsuoka S., Hryshko L.V., Nicoll D.A., Bershon M.M.,
RA
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RA

Burke E.P., Lifton R.P., Philipson K.D.;

```
RT
     "Cloning of the NCX2 isoform of the plasma membrane Na(+)-Ca2+
RT
    exchanger.";
RL
    J. Biol. Chem. 269:17434-17439(1994).
RN
    TISSUE SPECIFICITY.
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    STRAIN=Sprague-Dawley;
RC
    MEDLINE=96394663; PubMed=8798769;
RX
    Nicoll D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
RA
    Philipson K.D.;
RA
RT
    "Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.";
RL
    J. Biol. Chem. 271:24914-24921(1996).
CC
    -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC
        coupling. Ca(2+) is extruded from the cell during relaxation so as
CC
        to prevent overloading of intracellular stores.
CC
    -!- ENZYME REGULATION: By ATP.
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
    -!- TISSUE SPECIFICITY: Brain and skeletal muscle.
    -----
CC
CC
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    between the Swiss Institute of Bioinformatics and the EMBL outstation -
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    the European Bioinformatics Institute. There are no restrictions on its
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    or send an email to license@isb-sib.ch).
CC
    ______
DR
    EMBL; U08141; AAA19920.1; -.
DR
    PIR; A54139; A54139.
DR
    InterPro; IPR003644; Calx beta.
DR
    InterPro; IPRO04836; Na Ca Ex.
    InterPro; IPR004837; NaCa Exmemb.
DR
    Pfam; PF03160; Calx-beta; 2.
DR
    Pfam; PF01699; Na Ca Ex; 2.
DR
DR
    PRINTS; PR01259; NACAEXCHNGR.
DR
    SMART; SM00237; Calx beta; 2.
    TIGRFAMs; TIGR00845; caca; 1.
DR
KW
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KW
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KW
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                 21
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                69
FT
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FT
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FT
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FT
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                220
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FT
    TRANSMEM
                223
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FT
    DOMAIN
                247
                      720
                                CYTOPLASMIC (POTENTIAL).
FT
    TRANSMEM
                721
                      740
                                POTENTIAL.
FT
    DOMAIN
                741
                      747
                                EXTRACELLULAR (POTENTIAL).
FT
    TRANSMEM
                748
                      770
                                POTENTIAL.
FT
    DOMAIN
                771
                      772
                                CYTOPLASMIC (POTENTIAL).
    TRANSMEM
               773
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                               POTENTIAL.
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FT
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FΤ
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                             POTENTIAL.
FT
    DOMAIN
              844
                    854
                             CYTOPLASMIC (POTENTIAL).
FT
    TRANSMEM
              855
                    875
                             POTENTIAL.
              876
                    892
FT
    DOMAIN
                            EXTRACELLULAR (POTENTIAL).
    TRANSMEM
              893
                    909
FT
                             POTENTIAL.
FT
    DOMAIN
              910
                    921
                            CYTOPLASMIC (POTENTIAL).
    DOMAIN
              248
FT
                    267
                            CALMODULIN-BINDING (BY SIMILARITY).
FT
    REPEAT
              135
                    175
                            ALPHA-1.
FT
    REPEAT
              397
                    468
                            BETA-1.
FT
              527
                    597
                            BETA-2.
    REPEAT
FT
    REPEAT
              790
                    826
                            ALPHA-2.
               29
                     32
FT
    DOMAIN
                            POLY-PRO.
FT
    DOMAIN
              638
                    641
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FT
    CARBOHYD
               34
                     34
                            N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
              817
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                            N-LINKED (GLCNAC. . .) (POTENTIAL).
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 Best Local Similarity
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                                              Indels
                                                      34;
                                                                 9;
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Qу
            || : :|
                      1:
                              Db
         21 EATPTPSLPPPPANDSDASPGGCQGSYRCQPGVLLPVWEPDDPSLGDKAARAVVYFVAMV 80
Qу
         86 YMFLGVSIIADRFMASIEVITSOEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSA 145
            81 YMFLGLSIIADRFMASIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSA 140
Db
        146 PEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFI 205
Qу
            141 PEILLSVIEVCGHNFQAGELGPGTIVGSAAFNMFVVIAVCVYVIPAGESRKIKHLRVFFV 200
Db
        206 TAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKY 265
Qу
            201 TASWSIFAYVWLYLILAVFSPGVVQVWEALLTLVFFPVCVVFAWMADKRLLFYKYVYKRY 260
Db
        266 RTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGNL-----VPLEGKEVDESRREMIRIL 320
Qу
                | | | :|:| |||:|:||
        261 RTDPRSGIIIGAEGDPPKSIELDGTFVGTE-VPGELGALGTGPAEARELDASRREVIQIL 319
Db
        321 KDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKA 380
Qу
            Db
        320 KDLKQKHPDKDLEQLVGIAKYYALLHQQKSRAFYRIQATRLMTGAGNVLRRHAADAARRP 379
        381 SSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSA 440
Qу
                  380 GA-NDGAPDDEDDGASRIFFEPSLYHCLENCGSVLLSVACOGGEGNSTFYVDYRTEDGSA 438
Db
Qу
        441 NAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEO----PEE 496
            439 KAGSDYEYSEGTLVFKPGETQKELRIGIIDDDIFEEDEHFFVRLLNLRVGDAQGMFEPDG 498
Db
        497 GMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTS 556
Qу
                      :|||| :| ::|:|:|:|
        499 G-----GRPKGRLVAPLLATVTILDDDHAGIFSFQDRLLHVSECMGTVDVRVVRSS 549
Db
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557 GARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFI 616
Qy
            550 GARGTVRLPYRTVDGTARGGGVHYEDACGELEFGDDETMKTLQVKIVDDEEYEKKDNFFI 609
Db
        617 ALGEPKWMERGISDVT-----DRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEF 670
Qу
             11:1:1::1111 :
                               610 ELGQPQWLKRGISALLLNQGDGDRKLTAEEEEAQRIAEMGKPVLGENCRLEVIIEESYDF 669
Db
        671 KTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESG--EERLPSCFDYVMHF 728
Qу
            Db
        670 KNTVDKLIKKTNLALVIGTHSWREQFLEAVTVS-AGDEEEDEDGSREERLPSCFDYVMHF 728
        729 LTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVF 788
Qy . .
            729 LTVFWKVLFACLPPTEYCHGWACFGVCILVIGLLTALIGDLASHFGCTVGLKDSVNAVVF 788
Db
        789 VAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEF 848
Qу
            789 VALGTSIPDTFASKVAALQDQCADASIGNVTGSNAVNVFLGLGVAWSVAAVYWAVQGRPF 848
Db
        849 HVSAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYIL 908
Qу
               849 EVRTGTLAFSVTLFTVFAFVGIAVLLYRRRPHIGGELGGPRGPKLATTALFLGLWFLYIL 908
Db
        909 FATLEAYCYIKGF 921
Qv
            11:1111:1:11
Db
        909 FASLEAYCHIRGF 921
RESULT 12
NKX1 BOVIN
    NKX1 BOVIN
TD
                 STANDARD;
                              PRT; 1216 AA.
AC
    028139; 046384;
DT
    28-FEB-2003 (Rel. 41, Created)
DT
    28-FEB-2003 (Rel. 41, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DE
    Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-
DE
    exchange protein 1) (Retinal rod Na-Ca+K exchanger).
    SLC24A1 OR NCKX1.
GN
os
    Bos taurus (Bovine).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
    Bovidae; Bovinae; Bos.
    NCBI TaxID=9913;
OX
RN
RP
    SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 66-88; 232-249;
    647-660 AND 1119-1136.
RP
    TISSUE=Retina;
RC
RX
    MEDLINE=92258377; PubMed=1582405;
    Reilaender H., Achilles A., Friedel U., Maul G., Lottspeich F.,
RA
RA
    Cook N.J.;
    "Primary structure and functional expression of the Na/Ca, K-exchanger
RT
RT
    from bovine rod photoreceptors.";
RL
    EMBO J. 11:1689-1695(1992).
RN
    [2]
    SEQUENCE OF 725-1216 FROM N.A. (ISOFORM 1).
```

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RC
     TISSUE=Retina;
     MEDLINE=98138491; PubMed=9478004;
RX
     Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.M.;
RA
RT
     "cDNA cloning of the human retinal rod Na-Ca + K exchanger:
RT
     comparison with a revised bovine sequence.";
RL
     Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
CC
     -!- FUNCTION: Critical component of the visual transduction cascade,
CC
         controlling the calcium concentration of outer segments during
CC
         light and darkness. Light causes a rapid lowering of cytosolic
CC
         free calcium in the outer segment of both retinal rod and cone
CC
         photoreceptors and the light-induced lowering of calcium is caused
CC
         by extrusion via this protein which plays a key role in the
CC
         process of light adaptation. Transports one Ca(2+) and one K(+) in
CC
         exchange for four Na(+) (By similarity).
CC
     -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
    -!- ALTERNATIVE PRODUCTS:
CC
         Event=Alternative splicing; Named isoforms=2;
CC
         Name=1;
CÇ
           IsoId=Q28139-1; Sequence=Displayed;
CC
         Name=2;
CC
           IsoId=Q28139-2; Sequence=VSP 006159;
CC
           Note=No experimental confirmation available;
CC
    -!- TISSUE SPECIFICITY: Retina.
CC
     -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC
CC
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CC
    or send an email to license@isb-sib.ch).
     ______
CC
DR
    EMBL; X66481; CAA47108.1; -.
DR
    EMBL; AF025664; AAB88884.1; -.
DR
    PIR; S20969; S20969.
    InterPro; IPR004817; K_NaCaexchang.
DR
DR
    InterPro; IPR004481; K NaCaexchng.
    InterPro; IPR004837; NaCa Exmemb.
DR
    Pfam; PF01699; Na Ca Ex; \overline{2}.
    TIGRFAMs; TIGR00927; 2A1904; 1.
DR
DR
    TIGRFAMs; TIGR00367; TIGR00367; 1.
KW
    Vision; Transport; Antiport; Symport; Calcium transport;
KW
     Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
    Phosphorylation; Signal; Repeat; Alternative splicing.
KW
FT
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                  1
                        38
                                  POTENTIAL.
    CHAIN
                 39
                                  SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
FT
                      1216
                 39
FT
    DOMAIN
                       446
                                 EXTRACELLULAR (POTENTIAL).
                447
FT
    TRANSMEM
                       467
                                 POTENTIAL.
    DOMAIN
                468
                       491
FT
                                 CYTOPLASMIC (POTENTIAL).
FT
    TRANSMEM
                492
                       512
                                 POTENTIAL.
                513
FT
    DOMAIN
                       518
                                 EXTRACELLULAR (POTENTIAL).
FT
    TRANSMEM
                519
                       539
                                 POTENTIAL.
FT
    DOMAIN
                540
                       557
                                 CYTOPLASMIC (POTENTIAL).
FT
    TRANSMEM
                558
                       578
                                 POTENTIAL.
FT
    DOMAIN
                579
                       579
                                 EXTRACELLULAR (POTENTIAL).
FT
                580
                       600
    TRANSMEM
                                 POTENTIAL.
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601
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    DOMAIN
                    1024
                             CYTOPLASMIC (POTENTIAL).
             1025 1045
FT
    TRANSMEM
                             POTENTIAL.
FT
    DOMAIN
             1046 1052
                             EXTRACELLULAR (POTENTIAL).
FT
    TRANSMEM
             1053 1073
                             POTENTIAL.
             1074 1088
FT
    DOMAIN
                             CYTOPLASMIC (POTENTIAL).
             1089 1109
1110 1127
FT
    TRANSMEM
                             POTENTIAL.
FT
    DOMAIN
                             EXTRACELLULAR (POTENTIAL).
    TRANSMEM 1128 1148
FT
                             POTENTIAL.
FT
    DOMAIN
             1149 1157
                             CYTOPLASMIC (POTENTIAL).
             1158 1178
FT
    TRANSMEM
                             POTENTIAL.
             1179 1185
FT
    DOMAIN
                             EXTRACELLULAR (POTENTIAL).
             1186 1206
\mathbf{FT}
    TRANSMEM
                             POTENTIAL.
FT
    DOMAIN
             1207
                   1216
                             CYTOPLASMIC (POTENTIAL).
    DOMAIN
             796 928
FT
                             8 X 17 AA TANDEM REPEATS OF D-E-D-E-G-E-
FT
                             I-Q-A-G-E-[GA]-G-E-V-[EK]-G.
FT
    REPEAT
              796 811
                             1 (APPROXIMATE).
FT
    REPEAT
              812
                    828
                             2.
FT
    REPEAT
              829
                    845
                             3.
              846
FT
    REPEAT
                    862
                             4.
                  879
FT
              863
    REPEAT
                             5.
\mathbf{FT}
              880 896
   REPEAT
                             6.
              897 913
FT
   REPEAT
                             7.
FT
   REPEAT
              914 928
                            8 (APPROXIMATE).
FT
   REPEAT
              488 528
                             ALPHA-1.
             1096 1127
   REPEAT
FT
                             ALPHA-2.
             984 1009
    DOMAIN
FT
                             POLY-GLU.
              652 652
    MOD RES
FT
                             PHOSPHORYLATION (POTENTIAL).
FT
   CARBOHYD
             290 290
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
    CARBOHYD 303 303
FT
                             N-LINKED (GLCNAC. . .) (POTENTIAL).
             868 884
FT
    VARSPLIC
                             Missing (in isoform 2).
                             /FTId=VSP 006159.
FT
              84 84
FT
    CONFLICT
                             MISSING (IN REF. 1; AA SEQUENCE).
              234
                             MISSING (IN REF. 1; AA SEQUENCE).
FT
    CONFLICT
                    234
             244
                    245
                            MISSING (IN REF. 1; AA SEOUENCE).
\mathbf{FT}
    CONFLICT
             244 245
857 857
    CONFLICT
FΨ
                            A \rightarrow G (IN REF. 2).
SO
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                      6.4%; Score 306.5; DB 1; Length 1216;
 Query Match
 Best Local Similarity 21.4%; Pred. No. 1e-11;
 Matches 202; Conservative 113; Mismatches 324; Indels 305; Gaps 38;
         77 VIVYFVALIYMFLGVSIIADR-FMASIEVITSOEREVTIKKPNGETSTTTIRVWNETVSN 135
Qy
            1::: ::|:|: :: : | | | : : : | | | :
Db
        449 VVLHIFGMMYVFVALAIVCDEYFVPALGVITDK------LQI-SEDVAG 490
        136 LTLMALGSSAPEILLSLIEVCGHGFIA-GDLGPSTIVGSAAFNMFIIIGICVYVIPDGET 194
Qу
            491 ATFMAAGGSAPELFTSLIGV----FISHSNVGIGTIVGSAVFNILFVIGTCALF----S 541
Db
        195 RKIKHLRVFFITAAWSIFAYIWLY-----MILAVFSPGVVQVWEGLLTLFFFPVCVL-LA 248
Qу
           542 REILNL----TWWPLFRDITFYIFDLMMLILFFLDSLIAWWESVLLLLAYAFYVFTMK 595
Db
Qу
        249 WVADKRLLFYKYMHKK-----YRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDG 299
           Db
        596 WNQQLELWVKEQLNKRPVAKVMALGDLSKPGDGTVVVDEQQDNKKLKLSSMLTRG---S 651
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300 NLVPLEGKEVDESRRE-MIRILKDLKQKHPEKDLDQ--LVEMANYYALSHQQKSRAFYRI 356
Qу
          Db
        652 SSASLHNSTIRSTIYQLMLHSLDPLGEARPSKDKEEETLIPEAK----- 695
        357 QATRMMTGAGNILKKHAAEOAKKASSMSEVHTDEPE-----DFISKVFFDPCSYOC 407
Qу
                 696 -----ATPQAKAESKPEEEPAKLPEVTVTPAPAPDVKGDQEEDPGSQGV 739
Db
        408 ---LENCG-----AVLLTVVRKGGDMSKTMYVDYKTEDGS----ANAGADYEFT 449
Qу
             740 GAEAENTGERTGGEAEAPAEGENGERSGGDAALGGESEGKAENESEGDIPAERRGDDE-D 798
Db
        450 EGTVVLKPGETQKEFSVGII-----DDDIFE-----EDEHFFVRLSNV 487
Qу
           11::11::11
                                  1:1
        799 EGEIQAEGGEVKGDEDEGEIQAGEGGEVEGDEDEGEIQAGEGGEVEGDEDEGEIQAGEAG 858
        488 RIEEEQPE-----EGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFEC 536
Qу
            :1 :: 1
                                                 1:1 1
                                         -----DEDEGEIQAGEA 891
Db
        859 EVEGDEDEGEIQAGEGGEVEG-----
        537 DTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGG-----GEDFEDTYGELEFK 590
Qу
            892 GEVEGDEDEGEIQ-----AGEGGEV----KGDEGEIQAGEAGEVEGED-----GEVEGG 936
Db
Qу
        591 NDETVKTIRVKIVDEEEYERQENFFIALGEPKWMERGI-----SDVTDRKLTMEEEE 642
           937 EDE--GEIQAGEGGEGETGEQELNAEIQGEAKDDEEGVDGEGGGDGGDSEDEEEEDEEE 994
Db
Qу
        643 AKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDOFMEAITV 702
                            11 1
       995 D------EEEEE-----
Db
        703 SAAGDEDESGEERLPSCFDY------VMHFLTVFWKVLFACVPPTEYCHGWACFAV 754
Qу
              :|:|:| | | |: |: |: |: |: |: |:
       1001 ----EEEEEEEEEEPEQPLSLEWPETRRKQAIYLFLLPIVFPLWLTVPDVRRLEAKKFFVI 1056
Db
        755 ----SILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALODVY 810
Qу
              1057 TFLGSILWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGL- 1115
Db
        811 ADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCI 870
Qy
            Db
       1116 GDMAVSSSVGSNIFDITVGLPLPWMLFSLINGLQPVAVS-SNGLFCAIVLLFLMLLFVIS 1174
       871 SVLLYRRRPHLGGELGGPRGCKLATTW----LFVSLWLLYILF 909
Qy
                         | | | | | | | | | | | | | | |
       1175 SIAL----CK---WRMNKILGFTMFLLYFVF 1198
Db
RESULT 13
NKX1 RAT
  NKX1_RAT STANDARD; PRT; 1181 AA.
   Q9QZM6; Q62932;
   28-FEB-2003 (Rel. 41, Created)
   28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DT
    Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-
```

```
DE
    exchange protein 1) (Retinal rod Na-Ca+K exchanger).
GN
    SLC24A1 OR NCKX1.
OS
    Rattus norvegicus (Rat).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX
    NCBI TaxID=10116;
RN
    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP
RC
    STRAIN=Sprague-Dawley; TISSUE=Eye;
    MEDLINE=20217335; PubMed=10751314;
RX
RA
    Poon S., Leach S., Li X.-F., Tucker J.E., Schnetkamp P.P.M.,
RA
    Lvtton J.;
RT
    "Alternatively spliced isoforms of the rat eye
RT
    sodium/calcium+potassium exchanger NCKX1.";
RL
    Am. J. Physiol. 278:C651-C660(2000).
RN
    SEQUENCE OF 1067-1155 FROM N.A.
RP
RA
    White K.E., Gesek F.A., Friedman P.A.;
RL
    Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
CC
    -!- FUNCTION: Critical component of the visual transduction cascade,
CC
        controlling the calcium concentration of outer segments during
CC
        light and darkness. Light causes a rapid lowering of cytosolic
CC
        free calcium in the outer segment of both retinal rod and cone
CC
        photoreceptors and the light-induced lowering of calcium is caused
CC
        by extrusion via this protein which plays a key role in the
CC
        process of light adaptation. Transports one Ca(2+) and one K(+) in
CC
        exchange for four Na(+).
    -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC
    -!- ALTERNATIVE PRODUCTS:
CC
        Event=Alternative splicing; Named isoforms=4;
CC
        Name=1:
CC
          IsoId=Q9QZM6-1; Sequence=Displayed;
CC
        Name=2;
CC
          IsoId=Q9QZM6-2; Sequence=VSP 006161;
CC
CC
          IsoId=Q9QZM6-3; Sequence=VSP 006162;
CC
CC
          IsoId=Q9QZM6-4; Sequence=VSP 006163;
CC
    -!- TISSUE SPECIFICITY: Highly expressed in the eye.
CC
    -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC
    ------
CC
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    or send an email to license@isb-sib.ch).
    ______
CC
    EMBL; AF176688; AAD53121.1; -.
DR
DR
    EMBL; U49235; AAB37753.1; -.
DR
    InterPro; IPR004817; K NaCaexchang.
DR
    InterPro; IPR004481; K NaCaexchng.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
    Pfam; PF01699; Na Ca Ex; 2.
    TIGRFAMs; TIGR00927; 2A1904; 1.
DR
DR
    TIGRFAMs; TIGR00367; TIGR00367; 1.
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KW
    Vision; Transport; Antiport; Symport; Calcium transport;
    Transmembrane; Glycoprotein; Phosphorylation; Signal; Repeat;
KW
    Alternative splicing.
KW
FT
    SIGNAL
                 1
                                 POTENTIAL.
\mathbf{FT}
    CHAIN
                 39
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                                 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
                       419
FΤ
    DOMAIN
                 39
                                 EXTRACELLULAR (POTENTIAL).
                420
FT
    TRANSMEM
                       440
                                 POTENTIAL.
                                 CYTOPLASMIC (POTENTIAL).
FT
    DOMAIN
                441
                       464
    TRANSMEM
FT
                465
                     485
                                 POTENTIAL.
FT
    DOMAIN
                486
                       491
                                 EXTRACELLULAR (POTENTIAL).
FT
    TRANSMEM
                492
                       512
                                 POTENTIAL.
                513
FT
    DOMAIN
                       519
                                 CYTOPLASMIC (POTENTIAL).
    TRANSMEM
                520
                       544
FT
                                 POTENTIAL.
                545
                       552
FT
    DOMAIN
                                 EXTRACELLULAR (POTENTIAL).
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                                 POTENTIAL.
                570
                      989
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FT
    DOMAIN
                990
FT
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                                 POTENTIAL.
               1011
\mathbf{FT}
    DOMAIN
                      1017
                                 EXTRACELLULAR (POTENTIAL).
                      1038
FT
    TRANSMEM
               1018
                                 POTENTIAL.
               1039 1053
FT
    DOMAIN
                                 CYTOPLASMIC (POTENTIAL).
               1054 1074
FT
    TRANSMEM
                                 POTENTIAL.
FT
    DOMAIN
               1075 1092
                                 EXTRACELLULAR (POTENTIAL).
FT
    TRANSMEM
               1093 1113
                                 POTENTIAL.
               1114
FT
                      1121
                                 CYTOPLASMIC (POTENTIAL).
    DOMAIN
               1122
FT
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                      1142
                                 POTENTIAL.
               1143
FT
    DOMAIN
                      1150
                                 EXTRACELLULAR (POTENTIAL).
               1151
FT
    TRANSMEM
                      1171
                                 POTENTIAL.
               1172
FT
                      1181
    DOMAIN
                                 CYTOPLASMIC (POTENTIAL).
FT
    REPEAT
               461
                      501
                                 ALPHA-1.
               1061
                      1092
FT
    REPEAT
                                 ALPHA-2.
FT
    DOMAIN
                730
                      905
                                 14 X APPROXIMATE TANDEM REPEATS.
FT
                730
                       741
    REPEAT
FT
    REPEAT
                742
                       754
                                 2.
FT
    REPEAT
                755
                       766
                                 3.
FT
                767
                       778
    REPEAT
                                 4.
FT
                779
                       791
    REPEAT
                                 5.
FT
    REPEAT
                792
                       804
                                 6.
FT
                805
                       817
    REPEAT
                                 7.
FT
                818
                       830
    REPEAT
                                 8.
FT
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                       843
                                 9.
    REPEAT
FT
    REPEAT
                844
                       856
                                 10.
FT
                857
                       869
    REPEAT
                                 11.
FT
                870
                       881
    REPEAT
                                 12.
                       893
FT
                882
                                 13.
    REPEAT
FT
    REPEAT
                894
                       905
                                 14.
FT
    DOMAIN
                952
                       974
                                 POLY-GLU.
FT
    MOD RES
                625
                       625
                                 PHOSPHORYLATION (POTENTIAL).
FT
    CARBOHYD
                271
                       271
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
                                 Missing (in isoform 2).
    VARSPLIC
                598
                       710
FT
                                 /FTId=VSP 006161.
FT
    VARSPLIC
               616
                       710
                                 Missing (in isoform 3).
FT
                                 /FTId=VSP 006162.
    VARSPLIC 652
                       679
\mathbf{FT}
                                 Missing (in isoform 4).
FT
                                 /FTId=VSP 006163.
    SEQUENCE 1181 AA; 129980 MW; B063C1C1193696AE CRC64;
SQ
 Query Match 6.3%; Score 303.5; DB 1; Length 1181;
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Matches		Similarity 20.4%; Pred. No. 1.5e-11; 4; Conservative 131; Mismatches 305; Indels 321; Gaps	40;
Qу		VIVYFVALIYMFLGVSIIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN	
Db	422	::: : : : :: : : VVLHIFGMTYVFVALAIVCDEYFVPALGVITDKLQI-SEDVAG	463
Qу	136	LTLMALGSSAPEILLSLIEVCGHGFIA-GDLGPSTIVGSAAFNMFIIIGICVYVIPDGET	194
Db	464		514
Qу	195	RKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCV	245
Db	515	: : : :: :: :: REILNLTWWPLFRDVSFYILDLSMLIVFFLDSLIAWWESLLLLLAYALYVFTMK	568
Qу	246	LLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGK	290
Db	569	: :: ::: WNKQIERWVKEQLSRRPVAKVMALGDLSKPSDGAIEENEQQDNKKLKLPSVLTRGSSSAS	628
Qу	291	MMNSEGKEVDESRREMIRILKDLKQKHP	328
Db	629	: : : : : : : LHNSIIRSTIYHLMLHSLDPLGEARPSKDKQESLNQEARVLPQTKAESSSDEEEPAELPA	688
Qу	329	EKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGN	367
Db	689	:: : : : :::: :: ! VTVTPAPAPEDKGDQEEDPGCQEDVDEAEHRGDMTGEEGERETEAEGKKDEEGETE	744
Qу		ILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSK	
Db	745	: :: :	774
Qу	428	TMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFE	175
			413
Db	775	:: : :	
Db Qy		EQEGETEAEGKEADHEGETEAEGKEVEHEGETEAEGTEDEQEGETEAEGKEVEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVT	827
	476	EQEGETEAEGKEADHEGETEAEGKEVEHEGETEAEGTEDEQEGETEAEGKEVE	827 522
Qу	476 828	EQEGETEAEGKEADHEGETEAEGKEVEHEGETEAEGTEDEQEGETEAEGKEVEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVT	827 522 863
Qy Db	476 828 523	EQEGETEAEGKEADHEGETEAEGKEVEHEGETEAEGTEDEQEGETEAEGKEVEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVT	827522863582
Qy Db Qy	476 828 523 864	EQEGETEAEGKEADHEGETEAEGKEVEHEGETEAEGTEDEQEGETEAEGKEVEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVT	827522863582904
Qy Db Qy Db	476 828 523 864 583	EQEGETEAEGKEADHEGETEAEGKEVEHEGETEAEGTEDEQEGETEAEGKEVEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVT	827522863582904639
Qy Db Qy Db	476 828 523 864 583 905	EQEGETEAEGKEADHEGETEAEGKEVEHEGETEAEGTEDEQEGETEAEGKEVEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVT	827522863582904639956
Qy Db Qy Db Qy	476 828 523 864 583 905 640	EQEGETEAEGKEADHEGETEAEGKEVEHEGETEAEGTEDEQEGETEAEGKEVEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVT	827 522 863 582 904 639 956 699
Qy Db Cy Db Cy Db	476 828 523 864 583 905 640 957	EQEGETEAEGKEADHEGETEAEGKEVEHEGETEAEGTEDEQEGETEAEGKEVEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVT	827 522 863 582 904 639 956 699
Qy Db Cy Db Cy Db Cy Db	476 828 523 864 583 905 640 957 700	EQEGETEAEGKEADHEGETEAEGKEVEHEGETEAEGTEDEQEGETEAEGKEVEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVT	827 522 863 582 904 639 956 699 967 751

```
Db
        1019 FVITFLGSIIWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARK 1078
         808 DVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSA-GTLAFSVTLFTIFA 866
Qу
              _ | || :
         1079 GL-GDMAVSSSVGSNIFDITVGLPVPWLLFSLINAL--QPIPVSSNGLFCAIVLLFLMLL 1135
Db
         867 FVCISVLLYRRRPHLGGELGGPRGCKLATTW-----LFVSLWLLYILFATL 912
Qy
                                    11 1:
        1136 FVIFSI-----ASCK----WRMNKILGFTMFLLYFVFLVI 1166
Db
RESULT 14
NKX1 HUMAN
    NKX1 HUMAN
                   STANDARD;
                                  PRT; 1099 AA.
    060721; 043485; 075184;
    28-FEB-2003 (Rel. 41, Created)
DT
     28-FEB-2003 (Rel. 41, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
DE
    Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-
DE
    exchange protein 1) (Retinal rod Na-Ca+K exchanger).
GN
    SLC24A1 OR NCKX1 OR KIAA0702.
OS
    Homo sapiens (Human).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC
OX
    NCBI TaxID=9606;
RN
    [1]
RP
    SEQUENCE FROM N.A. (ISOFORM 1).
RC
    TISSUE=Retina;
RX
    MEDLINE=99072302; PubMed=9856482;
    Tucker J.E., Winkfein R.J., Murthy S.K., Friedman J.S., Walter M.A.,
RA
    Demetrick D.J., Schnetkamp P.P.M.;
RA
RT
     "Chromosomal localization and genomic organization of the human
RT
    retinal rod Na-Ca+K exchanger.";
    Hum. Genet. 103:411-414(1998).
RL
RN
    [2]
RP
    SEQUENCE FROM N.A. (ISOFORM 2).
RC
    TISSUE=Retina;
RX
    MEDLINE=98138491; PubMed=9478004;
RA
    Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.M.;
RT
     "cDNA cloning of the human retinal rod Na-Ca + K exchanger:
RT
     comparison with a revised bovine sequence.";
RL
    Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
RN
RP
    SEQUENCE OF 1-999 FROM N.A. (ISOFORM 2).
RC
    TISSUE=Brain;
RX
    MEDLINE=98403880; PubMed=9734811;
    Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA
    Kotani H., Nomura N., Ohara O.;
RA
    "Prediction of the coding sequences of unidentified human genes. X.
RT
RT
    The complete sequences of 100 new cDNA clones from brain which can
RT
    code for large proteins in vitro.";
RL
    DNA Res. 5:169-176(1998).
CC
     -!- FUNCTION: Critical component of the visual transduction cascade,
CC
        controlling the calcium concentration of outer segments during
CC
        light and darkness. Light causes a rapid lowering of cytosolic
CC
        free calcium in the outer segment of both retinal rod and cone
CC
        photoreceptors and the light-induced lowering of calcium is caused
```

```
CC
        by extrusion via this protein which plays a key role in the
CC.
        process of light adaptation. Transports one Ca(2+) and one K(+) in
CC
        exchange for four Na(+).
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
    -!- ALTERNATIVE PRODUCTS:
CC
        Event=Alternative splicing; Named isoforms=2;
CC
        Name=1;
CC
          IsoId=060721-1; Sequence=Displayed;
CC
CC
          IsoId=060721-2; Sequence=VSP 006160;
CC
          Note=No experimental confirmation available;
CC
    -!- TISSUE SPECIFICITY: Found only in the outer segments of retinal
CC
        rod photoreceptors.
CC
    -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC
    CC
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    between the Swiss Institute of Bioinformatics and the EMBL outstation -
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    the European Bioinformatics Institute. There are no restrictions on its
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    modified and this statement is not removed. Usage by and for commercial
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    or send an email to license@isb-sib.ch).
CC
DR
    EMBL; AF062921; AAC16732.1; -.
    EMBL; AF062922; AAC77912.1; -.
DR
    EMBL; AF026132; AAB97832.1; -.
DR
DR
    EMBL; AB014602; BAA31677.1; ALT SEQ.
DR
    Genew; HGNC:10975; SLC24A1.
DR
    MIM; 603617; -.
DR
    GO; GO:0019867; C:outer membrane; NAS.
    GO; GO:0008273; F:calcium, potassium:sodium antiporter activity; NAS.
DR
    GO; GO:0006816; P:calcium ion transport; NAS.
DR
    GO; GO:0009642; P:response to light intensity; NAS.
DR
    GO; GO:0007601; P:vision; NAS.
DR
    InterPro; IPR004817; K_NaCaexchang.
DR
DR
    InterPro; IPR004481; K_NaCaexchng.
DR
    InterPro; IPR004837; NaCa Exmemb.
DR
    Pfam; PF01699; Na Ca Ex; 2.
    TIGRFAMs; TIGR00927; 2A1904; 1.
DR
    TIGRFAMs; TIGR00367; TIGR00367; 1.
DR
KW
    Vision; Transport; Antiport; Symport; Calcium transport;
KW
    Transmembrane; Glycoprotein; Phosphorylation; Signal; Repeat;
KW
    Alternative splicing.
                 1
FT
    SIGNAL
                       38
                                POTENTIAL.
                     1099
FT
    CHAIN
                 39
                                SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
    DOMAIN
                39
                      452
FT
                               EXTRACELLULAR (POTENTIAL).
    TRANSMEM
                453
                      473
FT
                               POTENTIAL.
                474
FT
    DOMAIN
                      497
                               CYTOPLASMIC (POTENTIAL).
FT
    TRANSMEM
                498
                      518
                                POTENTIAL.
FT
    DOMAIN
                519 522
                               EXTRACELLULAR (POTENTIAL).
                523 543
FT
    TRANSMEM
                                POTENTIAL.
FT
                544
                      563
    DOMAIN
                                CYTOPLASMIC (POTENTIAL).
FT
    TRANSMEM
                564
                      584
                                POTENTIAL.
FT
    DOMAIN
                585
                     585
                               EXTRACELLULAR (POTENTIAL).
FT
                586 606
    TRANSMEM
                               POTENTIAL.
                607
FT
    DOMAIN
                      907
                               CYTOPLASMIC (POTENTIAL).
                908
FT
    TRANSMEM
                      928
                               POTENTIAL.
```

```
DOMAIN
FT
             929 935
                            EXTRACELLULAR (POTENTIAL).
FΤ
    TRANSMEM 936 956
                            POTENTIAL.
FT
    DOMATN
             957 971
                            CYTOPLASMIC (POTENTIAL).
    TRANSMEM 972 992
FT
                            POTENTIAL.
    DOMAIN 993 1010
TRANSMEM 1011 1031
FT
                            EXTRACELLULAR (POTENTIAL).
FΤ
                            POTENTIAL.
   DOMAIN
            1032 1039
ተጥ
                            CYTOPLASMIC (POTENTIAL).
   TRANSMEM 1040 1060
FT
                            POTENTIAL.
    DOMAIN
            1061 1068
\mathbf{FT}
                            EXTRACELLULAR (POTENTIAL).
   TRANSMEM 1069 1089
FT
                            POTENTIAL.
   DOMAIN 1090 1099
                            CYTOPLASMIC (POTENTIAL).
FT
            494 534
979 1010
    REPEAT
FT
                            ALPHA-1.
   REPEAT
FT
                           ALPHA-2.
            860 890
\mathbf{FT}
   DOMAIN
                          POLY-GLU.
            658 658
\mathbf{FT}
   MOD RES
                          PHOSPHORYLATION (POTENTIAL).
   CARBOHYD 290 290
                          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
   VARSPLIC 631
                          Missing (in isoform 2).
                  648
                           /FTId=VSP 006160.
FΤ
  CONFLICT 516 516
                           V \rightarrow I (I\overline{N} REF. 2).
FT
SQ SEQUENCE 1099 AA; 121374 MW; 3911856BB088B5FD CRC64;
 Query Match
                     6.1%; Score 293; DB 1; Length 1099;
 Best Local Similarity 21.7%; Pred. No. 6.4e-11;
 Matches 191; Conservative 122; Mismatches 268; Indels 298; Gaps 42;
        77 VIVYFVALIYMFLGVSIIADR-FMASIEVITSOEREVTIKKPNGETSTTTIRVWNETVSN 135
Qy
           1::: ::|:|: | |: :: ||| :
        455 VVLHVFGMMYVFVALAIVCDEYFVPALGVITDK-----LOI-SEDVAG 496
        136 LTLMALGSSAPEILLSLIEVCGHGFIA-GDLGPSTIVGSAAFNMFIIIGICVYVIPDGET 194
QУ
           Db
        497 ATFMAAGGSAPELFTSLIGV----FISHSNVGIGTIVGSAVFNILFVIGTCSLF----S 547
Qy
        195 RKIKHLRVFFITAAWSIFAYIWLY-----MILAVFSPGVVOVWEGLLTLFFFPVCVLLAW 249
           Db
        548 REILNL-----TWWPLFRDVSFYILDLIMLILFFLDSLIAWWESLL------LLLAY 593
        250 VADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEV 309
Qу
                 11:1::::::
        594 A-----FYVFTMK---WNKHIEVWVKEQ----- 613
Db
        310 DESRREMIRI--LKDLKQKHPEKDLDQLVEMANYYALSHOOKSRAFYRIOATRMMTGAGN 367
Qу
             [] : :: |:|| | | : |: |:: ::: ::|
Db
        614 -LSRRPVAKVMALEDL----SKPGDGAI-----AVDELQDNK---KLKLPSLLT---- 654
        368 ILKKHAAEQAKKASSMSEVHTDEPEDFISKVF---FDPCSYOCLENCGAVLLTVVRKGGD 424
Qy
                 1 11
        655 -----RGSSSTSLHNSTIRSTIYQLMLHSLDP-----LREVR---- 686
Db
        425 MSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETOKEFSVGIIDDDIFEEDEHFFVRL 484
Qу
           687 LAK-----EKEEESLNOGARAO-POAKAESKP----- 712
Db
Qу
       485 SNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDD--DHAGIFTFECDTIHVS 542
               Db
        713 ----EEEEPAK-LPAVTVTPAPVP-----DIKGDOKENPG----GOEDVAEA 750
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543 ESIGVMEVKVLRTSG-----ARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKND---E 593
Qу
            Db
        751 ESTGEMPGEEGETAGEGETEEKSGGETQPEGEGETETQGKGEECEDE-NEAEGKGDNEGE 809
        594 TVKTIRVKIVD----EEEYERQENFFIALGEPKWMERGISD--VTDRKLTMEEEEAKRIA 647
Qy
              Db
        810 DEGEIHAEDGEMKGNEGETESOELSAENHGEAKNDEKGVEDGGGSDGGDSEEEEEEEEE 869
        648 EMGKPVLGEHPKLEVIIEESYEFKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGD 707
Qу
           870 E-----EEEEEEEQEEEEEE------ 885
Db
        708 EDEDESGEERLPSCFDY------ 755
Qу
            1:1:1 1 1 1:
                                : ||
                                         1: 11
                                                       - 1
Db
       -886 EEEEEKGNEE-PLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGS 944
        756 ILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASI 815
Qу
            Db
        945 IMWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGL-GDMAV 1003
        816 GNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHVSAGTLAFSVTLFTIFAFVCISVLLY 875
Qу
            Db
       1004 SSSVGSNIFDITVGLPVPWLLFSLINGLQPVPVS-SNGLFCAIVLLFLMLLFVISSI--- 1059
        876 RRRPHLGGELGGPRGCKLATTW----LFVSLWLLYILF 909
Qу
                     11 1 :::111:1
       1060 -----ASCK----WRMNKILGFTMFLLYFVF 1081
RESULT 15
NKX3 MOUSE
    NKX3 MOUSE
               STANDARD; PRT; 645 AA.
    Q99PD7; Q99JR2; Q99PD8;
DT
    28-FEB-2003 (Rel. 41, Created)
DT
    28-FEB-2003 (Rel. 41, Last sequence update)
DT
    10-OCT-2003 (Rel. 42, Last annotation update)
DE
    Sodium/potassium/calcium exchanger 3 precursor (Na(+)/K(+)/Ca(2+)-
DE
    exchange protein 3).
    SLC24A3 OR NCKX3.
GN
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RP
    SEQUENCE FROM N.A.
    STRAIN=129/SvJ, and CD-1; TISSUE=Brain, and Embryonic stem cells;
    MEDLINE=21303617; PubMed=11294880;
RX
    Kraev A., Quednau B.D., Leach S., Li X.-F., Dong H., Winkfein R.,
RA
    Perizzolo M., Cai X., Yang R., Philipson K.D., Lytton J.;
RA
    "Molecular cloning of a third member of the potassium-dependent
RT
RT
    sodium-calcium exchanger gene family, NCKX3.";
RL
   J. Biol. Chem. 276:23161-23172(2001).
RN
RP
    SEQUENCE OF 323-645 FROM N.A.
RC
    TISSUE=Breast tumor;
RX
    MEDLINE=22388257; PubMed=12477932;
    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
```

```
RA
     Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA
     Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA
     Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
     Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA
RA
     Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA
     Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA
     Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA
     Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
     Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA
RA
    Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA
     Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA
    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
     Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA
RA
    Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA
    Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA
     Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT
     "Generation and initial analysis of more than 15,000 full-length
RT
    human and mouse cDNA sequences.";
RL
    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC
    -!- FUNCTION: Transports one Ca(2+) and one K(+) in exchange for four
CC
        Na(+) (By similarity).
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
    -!- TISSUE SPECIFICITY: Abundant in the brain. Highest levels found in
CC
        selected thalamic nuclei, hippocampal CA1 neurons and in layer IV
CC
        of the cerebral cortex.
CC
    -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC
    ______
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DR
    EMBL; AF314821; AAG60049.1; -.
DŔ
    EMBL; AF314822; AAG60050.1; -.
DR
    EMBL; BC005742; AAH05742.1; -.
DR
    MGD; MGI:2137513; Slc24a3.
DR
    GO; GO:0008273; F:calcium, potassium:sodium antiporter activity; IDA.
DR
    InterPro; IPR004481; K NaCaexchng.
DR
    InterPro; IPR004837; NaCa_Exmemb.
DR
    Pfam; PF01699; Na Ca Ex; \overline{2}.
DR
    TIGRFAMs; TIGR00367; TIGR00367; 1.
KW
    Transport; Antiport; Symport; Calcium transport; Potassium transport;
KW
    Sodium transport; Transmembrane; Glycoprotein; Signal; Repeat.
FT
    SIGNAL
                  1
                        43
                                 POTENTIAL.
FT
    CHAIN
                 44
                       645
                                 SODIUM/POTASSIUM/CALCIUM EXCHANGER 3.
                 44
FT
    DOMAIN
                       106
                                 EXTRACELLULAR (POTENTIAL).
    TRANSMEM
                107
                       127
FT
                                 POTENTIAL.
FT
    DOMAIN
                128
                       151
                                 CYTOPLASMIC (POTENTIAL).
FT
    TRANSMEM
                152
                       172
                                 POTENTIAL.
FT
    DOMAIN
                173
                       181
                                 EXTRACELLULAR (POTENTIAL).
FT
    TRANSMEM
                182
                       202
                                 POTENTIAL.
FT
    DOMAIN
                203
                       209
                                 CYTOPLASMIC (POTENTIAL).
FT
    TRANSMEM
                210
                       230
                                 POTENTIAL.
FT
    DOMAIN
                231
                       234
                                 EXTRACELLULAR (POTENTIAL).
```

```
FT
    TRANSMEM 235 255
                            POTENTIAL.
    DOMAIN
             256 486
                           CYTOPLASMIC (POTENTIAL).
FT
    TRANSMEM 487 507
                           POTENTIAL.
                          POTENTIAL.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

POTENTIAL.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

POTENTIAL.

EXTRACELLULAR (POTENTIAL).

ALPHA-1.

ALPHA-2.
              508 512
FT
    DOMAIN
             513 533
534 551
    TRANSMEM
FT
FT
   DOMAIN
   TRANSMEM 552 572
FT
  DOMAIN 573 582
FT
   TRANSMEM 583 603
FT
            604 617
FT
   DOMAIN
   TRANSMEM 618 638

DOMAIN 639 645

REPEAT 148 188

REPEAT 520 551

DOMAIN 424 430
FT
FT
FT
FT REPEAT
FT DOMAIN
                           ALPHA-2.
                           POLY-GLU.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL). FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 645 AA; 71914 MW; C62DEB6CB4A01C96 CRC64;
 Query Match
                     5.5%; Score 266; DB 1; Length 645;
 Best Local Similarity 19.1%; Pred. No. 1.7e-09;
 Matches 162; Conservative 94; Mismatches 216; Indels 374; Gaps 30;
        77 VIVYFVALIYMFLGVSIIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN 135
Qу
           109 VVLHVLCAMYMFYALAIVCDDFFVPSLEKICERLH------LSEDVAG 150
        136 LTLMALGSSAPEILLSLIEVCGHGFIA-GDLGPSTIVGSAAFNMFIIIGICVYVIPDGET 194
Qу
            Db
        151 ATFMAAGSSAPELFTSVIGV----FITKGDVGVGTIVGSAVFNILCIIGVCGLFA--GOV 204
       195 RKIKHLRVFFITAAW-----SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAW 249
Qу
                  Db
        205 VAL-----SSWCLLRDSIYYTLSVVALIVFIYDEKVSWWESLVLVLMYLIYIVI-- 253
        250 VADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEV 309
Qу
                      254 -----AGNMVNG--LANN-----AEI 284
Db
Qу
        310 DESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNIL 369
           1:1
        285 DDS----- 287
Db
        370 KKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTM 429
Qу
                                            11 1 :
        430 YVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRI 489
Qу
                              |:|| ::|:
        295 -----LLSAYPH 320
Db
        490 EEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVME 549
Qу
           Db
        321 QLSFSEAGLRIMITSHFP-PKTRLS----MASRMLINERQRLINSRAYTNGESEVAIKIP 375
Qy
       550 VKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYE 609
```

Db	376	IKHTVENGT-GPSSAPDRGVNGTRRDDIVAETDNETENE	413
Qy	610	RQENFFIALGEPKWMERGISDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYE ::	669
Db	414	NEDNENNESDEEEEE	428
Qу	670	FKTTVDKLIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGE-ERLP	719
Db	429	DEDDDEGPYTPFDPPSGKLETVK	451
Qy	720	SCFDYVMHFLTVFWKVLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFG	774
Db	452	WAFTWPLSFVLYFTVPNCNKPH-WEKWFMVTFASSTLWIAAFSYMMVWMVTIIG	504
Qy	7 75	CTIGLKDSVTAVVFVAFGTSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAW : : :	834
Db	505	YTLGIPDVIMGITFLAAGTSVPDCMASLIVARQGM-GDMAVSNSIGSNVFDILIGLGLPW	563
Qу	835	SVAAITLFTIFAF:::: :	867
Db	564	ALQTLAVDYGSYIRLNSRGLIYSVGLLLASVFVTVFGVHLNKWQLDKKLGCGCLFLYGVF	623
Qy	868	VCISVL 873 : ::	
Db	624	LCFSIM 629	

Search completed: June 24, 2004, 16:12:39 Job time: 22.3323 secs